

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:19:50 ; Search time 37 Seconds
(without alignments)
28.605 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFSELWTS 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 1328

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	50.0	10	2 C39191	hypothetical prote
2	24	40.0	7	2 PH1602	Ig H chain V-D-J r
3	23	38.3	10	2 T13838	cytochrome-c oxida
4	20	33.3	6	2 B34835	dnaA protein - Pse
5	20	33.3	11	2 S05002	corazonin - Americ
6	19	31.7	6	2 PT0519	T-cell receptor be
7	19	31.7	6	2 A43129	neuropeptide GNFPR
8	19	31.7	8	2 A41117	acetylcholinestera
9	19	31.7	9	2 S36850	Ig heavy chain V r
10	18	30.0	9	2 S07241	litorin - Rohde's
11	18	30.0	10	2 C41946	T-cell receptor ga
12	18	30.0	10	2 S33789	neuropeptide Pec-H
13	18	30.0	11	1 LFTWE	probable trpKG lea
14	18	30.0	11	2 S33300	probable substance
15	17.5	28.2	8	2 JS0315	leucokinin V - Mad
16	17	28.3	7	2 PT0586	T-cell receptor be
17	17	28.3	8	2 A44960	neuropeptide Led-C
18	17	28.3	8	2 S08995	hypertrehalosemic
19	17	28.3	8	2 A49823	adipokinetic hormo
20	17	28.3	8	2 A43976	hypertrehalosemic
21	17	28.3	8	2 B43976	hypertrehalosemic
22	17	28.3	8	2 A05169	neuropeptide M-1 -
23	17	28.3	10	2 A31571	hypertrehalosemic/
24	16	26.7	4	2 PT0661	T-cell receptor be
25	16	26.7	7	4 IS5382	hypothetical pepti
26	16	26.7	8	2 A32523	peptidyl-dipeptida
27	16	26.7	8	2 S11545	adipokinetic hormo
28	16	26.7	8	2 A61348	red pigment-concen
29	16	26.7	8	2 A28004	adipokinetic hormo

30	16	26.7	8	2 A39308	glycine reductase
31	16	26.7	9	2 A24244	adipokinetic hormo
32	16	26.7	9	2 PT0315	Ig heavy chain CRD
33	16	26.7	9	2 A43848	cell surface adhes
34	16	26.7	10	2 S08997	hypertrehalosemic
35	16	26.7	10	2 A60421	hypertrehalosemic
36	16	26.7	10	2 S08998	hypertrehalosemic
37	16	26.7	10	2 A26381	hypertrehalosemic
38	16	26.7	10	2 PT0322	Ig heavy chain CRD
39	16	26.7	10	2 T13976	cytochrome-c oxida
40	16	26.7	10	2 T17057	cytochrome-c oxida
41	16	26.7	10	2 T12303	cytochrome-c oxida
42	16	26.7	10	2 T14019	cytochrome-c oxida
43	16	26.7	10	2 T17060	cytochrome-c oxida
44	16	26.7	10	2 T14043	cytochrome-c oxida
45	16	26.7	10	2 T14054	cytochrome-c oxida

ALIGNMENTS

RESULT 1

C39191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C:Species: Bacteroides fragilis
C>Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C:Accession: C39191
R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tr
A:Reference number: A39191; MUID:91100280; PMID:1846135
A:Accession: C39191
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <SPE>
A:Cross-references: GB:M37699

Query Match 50.0%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFSSELWTS 11
DB 2 YFSREWTS 9

RESULT 2

PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1602
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less micr
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1602
A:Molecule type: DNA
A:Residues: 1-7 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 40.0%; Score 24; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SELWT 10
DB 3 SSLWT 7

RESULT 3

T13838

cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
 C:Species: mitochondrion Bipes biporus
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13838
 R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A>Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A:Reference number: 217789; MUID:97153826; PMID:9000757
 A:Accession: T13838
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <NAC>
 A:Cross-references: UNIPROT:P92576; EMBL:U71335; NID:g1753232; PID:g1753235; PIDN:AAB482
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: C01
 C:Keywords: mitochondrion; oxidoreductase

Query Match 38.3%; Score 23; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGSFSS 6
 DB 4 TRSFFS 9

RESULT 4
 B34835
 dnaA protein - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 C:Accession: B34835
 R:Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A>Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
 A:Reference number: A34835; MUID:90160310; PMID:2106132
 A:Accession: B34835
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <YEE>
 A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
 C:Keywords: DNA binding

Query Match 33.3%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ELW 9
 DB 4 ELW 6

RESULT 5
 S05002
 corazonin - American cockroach
 C:Species: Periplaneta americana (American cockroach)
 C>Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
 C:Accession: S05002
 R:Veenstra, J.A.
 FEBS Lett. 250, 231-234, 1989
 A>Title: Isolation and structure of corazonin, a cardioactive peptide from the american
 A:Reference number: S05002; MUID:99325572; PMID:2753132
 A:Accession: S05002
 A:Molecule type: protein
 A:Residues: 1-11 <VEE>
 A:Cross-references: UNIPROT:P11496
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (gln) #status experimental
 F:1/Modified site: amidated carboxyl end (asn) #status experimental

Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELWTS 11
 DB 5 YSRGWTN 11

RESULT 6
 PT0519
 T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0519
 R:Peeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0519
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-6 <PEE>
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 31.7%; Score 19; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SELW 9
 DB 2 SSLW 5

RESULT 7
 A43129
 neuropeptide GNFRFamide - tapeworm (Moniezia expansa)
 C:Species: Moniezia expansa
 C>Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
 C:Accession: A43129
 R:Maule, A.; Shaw, C.; Halton, D.; Thim, L.
 Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
 A>Title: GNFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t
 A:Reference number: A43129; MUID:93312289; PMID:8323531
 A:Accession: A43129
 A:Molecule type: protein
 A:Residues: 1-6 <MAU>
 A:Cross-references: UNIPROT:P41966
 C:Keywords: amidated carboxyl end; neuropeptide
 F:6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 31.7%; Score 19; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSFF 5
 DB 1 GNFF 4

RESULT 8
 A41117
 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
 C:Species: Naja naja oxiana (Asian cobra, Oxus cobra)
 C>Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
 C:Accession: A41117
 R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A>Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo
 A:Reference number: A41117; MUID:91296772; PMID:2068091
 A:Accession: A41117
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <KRE>

A;Cross-references: UNIPROT:Q7LZ27
C;Keywords: carboxylic ester hydrolase

Query Match 31.7%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SELW 9
:|:
Db 2 AEMW 5

RESULT 9

S36850
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C;Accession: S36850
R;Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)
A;Reference number: S25024
A;Accession: S36850
A;Status: Preliminary
A;Molecule type: nucleic acid
A;Residues: 1-9 <JAC>
A;Cross-references: EMBL:X67387; NID:G50113; PIDN:CAA47799.1; PID:e51594; PID:gl333871
C;Keywords: heterotetramer; immunoglobulin

Query Match 31.7%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSFF 5
||:
Db 6 GSYF 9

RESULT 10

S07241
litorin - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Accession: S07241
R;Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer, P.EBS Lett. 182 53-56 1985
A;Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.
A;Reference number: S07241; MUID:85127560; PMID:3838283
A;Accession: S07241
A;Molecule type: protein
A;Residues: 1-9 <BAR>

A;Cross-references: UNIPROT:P08946
C;Superfamily: gastrin-releasing peptide
C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 30.0%; Score 18; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ELWTS 11
:|:
Db 1 QLWAT 5

RESULT 11

C41946
T-cell receptor gamma chain (1t.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C41946
A;Status: Preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <WHE>
C;Keywords: T-cell receptor

Query Match 30.0%; Score 18; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.9e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELWTS 11
:|:
Db 1 YCAVWS 7

RESULT 12

S53789
neuropeptide Pec-HrTH - Platyleura capensis
C;Species: platyleura capensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S53789
R;Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalose
A;Reference number: S53789; MUID:95225985; PMID:7710694
A;Accession: S53789
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:Q7M465
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 30.0%; Score 18; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELW 9
||:
Db 4 FSPSW 8

RESULT 13

LPTWWE
probable trpEG leader peptide - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S03315
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A;Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and
A;Reference number: S03315; MUID:89000781; PMID:2844259
A;Accession: S03315
A;Molecule type: DNA
A;Residues: 1-11 <SAT>
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262
A;Note: the source is designated as Thermus thermophilus HB8
C;Genetics:
A;Gene: trpL
C;Superfamily: probable trpEG leader peptide

Query Match 30.0%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SELW 9
:|:
Db 5 SALW 8

RESULT 14

S33300

probable substance P - smaller spotted catshark
 C:Species: Scylliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S33300
 R:Waugh, D.; Wang, Y.; Hazen, N.; Balment, R.J.; Conlon, J.M.
 Eur. J. Biochem. 214, 469-474, 1993
 A:Title: Primary structures and biological activities of substance-P-related peptides fr
 A:Reference number: S33300; MUID:93292508; PMID:7685693
 A:Accession: S33300
 A:Molecule type: protein
 A:Residues: 1-11 <WAU>
 A:Cross-references: UNIPROT:P41333
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and gas
 A:Note: substance P is derived by post-translational processing of preprotachykinin A
 C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 30.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSFF 5
 | | |
 Db 5 GQFF 8

RESULT 15
 JS0315
 leucokinin V - Madeira cockroach
 C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: JS0315
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A:Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
 A:Reference number: JS0315
 A:Accession: JS0315
 A:Molecule type: protein
 A:Residues: 1-8 <HOL>
 A:Cross-references: UNIPROT:P19987
 C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.2%; Score 17.5; DB 2; Length 8;
 Best Local Similarity 62.5%; Pred. No. 2.8e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 GSFSELW 9
 | | | | |
 Db 1 GSGFSS-W 7

Search completed: April 27, 2005, 15:30:31
 Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:18:52 ; Search time 173 Seconds
(without alignments)
32.560 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFSELWTS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	40.0	11	2	077895 oreochromis
2	24	40.0	11	2	077896 oreochromis
3	23	38.3	10	2	P92576 bipes bipor
4	23	38.3	11	2	P83537 lactobacill
5	21	35.0	9	2	O95953 homo sapien
6	20	33.3	10	2	Q61A62 homo sapien
7	20	33.3	11	1	CA42_LITCI
8	20	33.3	11	1	COR2_PERAM
9	20	33.3	11	2	077894 oreochromis
10	20	33.3	11	2	077898 oreochromis
11	20	33.3	11	2	Q65CG7 sinalea tom
12	19	31.7	6	1	FARP_MONEX
13	19	31.7	8	2	Q99MN0 mus musculu
14	19	31.7	8	2	Q7LZ27 naia oxiana
15	19	31.7	10	2	Q9TR47 bos taurus
16	19	31.7	10	2	Q8SHC6 furcifer be
17	19	31.7	11	2	Q9UC46 homo sapien
18	18	30.0	9	1	L1TR_PHYRO
19	18	30.0	9	2	Q9H3Y3
20	18	30.0	9	2	Q8H9Z1
21	18	30.0	9	2	Q90350
22	18	30.0	10	1	AKHX_LOCMI
23	18	30.0	10	2	Q7M465 platypleura
24	18	30.0	10	2	Q8SHB1 rhampoleon
25	18	30.0	10	2	Q8SHB4 furcifer ve
26	18	30.0	10	2	Q8SHB7 furcifer ou
27	18	30.0	10	2	Q8SHC0 furcifer la
28	18	30.0	10	2	Q8SHC3 furcifer la
29	18	30.0	11	1	LPW_THETH
30	18	30.0	11	1	TKNA_SCYCA
31	18	30.0	11	2	Q9UEL0 homo sapien

32	17.5	29.2	8	1	LCK5_LEUMA
33	17.5	29.2	11	2	Q9GSZ2
34	17	28.3	8	1	HTF1_PERAM
35	17	28.3	8	1	HTF_TENMO
36	17	28.3	8	1	HTF_ZOPRU
37	17	28.3	8	2	Q40530
38	17	28.3	9	2	Q8WGE6
39	17	28.3	10	1	HTF_HELZE
40	17	28.3	10	2	LABA_JATMU
41	17	28.3	10	2	Q9TU33
42	17	28.3	10	2	Q7J5U5
43	17	28.3	11	1	CA22_LITCI
44	17	28.3	11	1	MHB1_KLEPN
45	17	28.3	11	2	Q90735

ALIGNMENTS

RESULT 1

ID	077895	PRELIMINARY;	PRT;	11	AA.
AC	077895;				
DT	01-NOV-1998	(TRENBLrel. 08, Created)			
DT	01-NOV-1998	(TRENBLrel. 08, Last sequence update)			
DT	01-DEC-2001	(TRENBLrel. 19, Last annotation update)			
DE	MHC class II B locus 12 (Fragment)				
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;				
OC	Cichlidae; Oreochromis.				
OX	NCBI_TaxID=8128;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98315113; PubMed=9649539;				
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,				
RA	Figueroa F., Sultmann H., Klein J.;				
RT	"Linkage relationships and haplotype polymorphism among cichlid MHC				
RT	class II B loci."				
RL	Genetics 149:1527-1537(1998).				
DR	EMBL; AF050005; AAC41344.1; -.				
FT	NON_TER	1			
FT	NON_TER	11			
SQ	SEQUENCE	11	AA;	1367	MM;
					3F47C9EA72045A3 CRC64;

Query Match 40.0%; Score 24; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY	4	FFSELWTS	11
Db	3	FWSILWVA	10

RESULT 2

ID	077896	PRELIMINARY;	PRT;	11	AA.
AC	077896;				
DT	01-NOV-1998	(TRENBLrel. 08, Created)			
DT	01-NOV-1998	(TRENBLrel. 08, Last sequence update)			
DT	01-DEC-2001	(TRENBLrel. 19, Last annotation update)			
DE	MHC class II B locus 12 (Fragment)				
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;				
OC	Cichlidae; Oreochromis.				
OX	NCBI_TaxID=8128;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98315113; PubMed=9649539;				
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,				

RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050006; AAC41345.1; -.
 FT NON TER 1 1
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

 Query Match 40.0%; Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 4 PFSELM 9
 | : | | |
 DB 3 FWSMLW 8

 RESULT 3
 P92576 PRELIMINARY; PRT; 10 AA.
 AC P92576;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COL;
 OS Bipes biporus (Baja worm lizard).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
 OX NCBI_TaxID=52188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 RT rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Repetition slippage may cause parallel evolution in the secondary
 RT structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 DR EMBL; U71335; AAB48271.1; -.
 DR FIR; T13838; T13838.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;

 Query Match 38.3%; Score 23; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 TGSFES 6
 | : | | | |
 DB 4 TRSPFS 9

 RESULT 4
 P83537 PRELIMINARY; PRT; 11 AA.
 AC P83537;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.

OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RX DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
 RA Draws O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 RT Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC -!- INDUCTION: By elevated hydrostatic pressure.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 CC protein is: 65 kDa.
 FT NON TER 1 1
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

 Query Match 38.3%; Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GSFFS 6
 | : | | | |
 DB 1 GSFFA 5

 RESULT 5
 O95953 PRELIMINARY; PRT; 9 AA.
 ID O95953;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Galactocerebrosidase (EC 3.2.1.46) (Fragment).
 GN Name=GALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lulli L., Torchiana E., Finocchiaro G.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77631; AAD15626.1; -.
 DR GO; GO:0004336; F:galactosylceramidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2AADC2C699C8 CRC64;

 Query Match 35.0%; Score 21; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.6e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 QY 2 GSFFSELM 9
 | : | | | |
 DB 2 GFNVADLW 9

 RESULT 6
 O6LA62 PRELIMINARY; PRT; 10 AA.
 ID O6LA62;
 AC O6LA62;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Amiloride-sensitive epithelial sodium channel gamma subunit
 DE (Fragment).
 GN Name=SCNN1G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96421599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
 RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;
 RT "Genomic organization and the 5' flanking region of the gamma subunit
 of the human amiloride-sensitive epithelial sodium channel.";
 RL J. Biol. Chem. 271:26062-26066(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98316780; PubMed=9654208;
 RA Ludwig M., Bolkenius U., Wickert L., Marynen P., Bidlingmaier P.;
 RT "Structural organization of the gene encoding the alpha-subunit of the
 human amiloride-sensitive epithelial sodium channel.";
 RL Hum. Genet. 102:576-581(1998).
 DR EMBL; Z92982; CAB07506.1; -.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON_TER 1
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1157 MW; DBAFF833733B05A2 CRC64;
 Query Match 33.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 9.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SPFSBLW 9
 Db 1 SVVSEKW 7
 RESULT 7
 CA42 LITCI
 ID CA42 LITCI STANDARD; PRT; 11 AA.
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litorea citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 mountains tree frog Litorea citropa. Part 1. Sequence determination
 using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray; RANGE=1-11;
 CC NOTE=Ref.1.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE NEG.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KW Hypotensive agent; Pyrrolidone carboxylic acid; Sulfation.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 4 4 Sulfotyrosine.
 FT MOD_RES 11 11 Phenylalanine amide.
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;
 Query Match 33.3%; Score 20; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGSFF 5
 Db 5 TGSHF 9
 RESULT 8
 CORZ PERAM
 ID CORZ PERAM STANDARD; PRT; 11 AA.
 AC P11456;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the
 American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved in
 the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Amidation; Direct protein sequencing; Neuropeptide;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 11 11 Asparagine amide.
 SQ SEQUENCE 11 AA; 1387 MW; C7CF32D6415AB46 CRC64;
 Query Match 33.3%; Score 20; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 1e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 FSELWTS 11
 Db 5 YSRGWTN 11
 RESULT 9
 O77894
 ID O77894 PRELIMINARY; PRT; 11 AA.
 AC O77894;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050004; AAC41343.1; -.
 FT NON_TER 1
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 2; Indels 1; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 4 FFSWLV 9
 Db 3 FWSIVW 8

RESULT 10
 Q77898 ID 077898 PRELIMINARY; PRT; 11 AA.
 AC 077898; PRT; 11 AA.
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050008; AAC41347.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 2; Indels 1; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 4 FFSWLV 9
 Db 3 FWSIVW 8

RESULT 11
 Q65CG7 ID Q65CG7 PRELIMINARY; PRT; 11 AA.
 AC Q65CG7;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Transcriptional activator (Fragment).
 GN Name=AC2;
 OS Sinaloa tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=71186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N13;
 RA Rojas A., Kvarnheden A., Rodriguez D., Valkonen J.P.T.;
 RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in
 Nicaragua."
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ508781; CAD48523.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1356 MW; 861BC90602D379D5 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+04; Mismatches 3; Indels 1; Gaps 0;
 Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 0;

QY 3 SFFSELWT 10

Db 4 SFWELFS 11

RESULT 12
 FARP_MONEX STANDARD; PRT; 6 AA.
 ID FARP_MONEX STANDARD; PRT; 6 AA.
 AC P41966;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRPamide-like neuropeptide GNFRFP-amide.
 OS Moniezia expansa (Sheep tapeworm).
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidae; Anoplocephalidae; Moniezia.
 OX NCBI_TaxID=28841;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93312289; PubMed=8323531;
 RA Maule A.G., Shaw C., Halton D.W., Thim L.;
 RT "GNFRFPamide: a novel FMRPamide-immunoreactive peptide isolated from
 the sheep tapeworm, Moniezia expansa."
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
 family.
 DR PIR; A43129; A43129.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 6 Phenylalanine amide.
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 31.7%; Score 19; DB 1; Length 6;
 Best Local Similarity 75.0%; Pred. No. 1.6e+06; Mismatches 1; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSFF 5
 Db 1 GNFF 4

RESULT 13
 Q99MNO ID. Q99MNO PRELIMINARY; PRT; 8 AA.
 AC Q99MNO;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Adenosine deaminase tRNA-specific 1 (Fragment).
 GN Name=Adat1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=21231131; PubMed=11331948;
 RA Maas S., Kim Y.G., Rich A.;
 RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
 tRNA synthetases."
 RL Mamm. Genome 12:387-393(2001).
 DR EMBL; AF328904; AAK19310.1; -.
 DR MGD; MGI:1353631; Adat1.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADCB376 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06; Mismatches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 LWTs 11
 Db 1 MWTA 4

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RESULT 14
Q7LZ27
ID Q7LZ27 PRELIMINARY; PRT; 8 AA.
AC Q7LZ27;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Acetylcholinesterase (EC 3.1.1.7), venom (Fragment).
OS Naja oxiana (Central Asian cobra) (Oxus cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=8657;
RN [1]
RP SEQUENCE.
RX MEDLINE=91296772; PubMed=2068091;
RA Kreienkamp H.J., Weise C., Raba R., Aaviksaar A., Hucho F.;
RT "Anionic subsites of the catalytic center of acetylcholinesterase from
RT Torpedo and from cobra venom.";
EL Proc. Natl. Acad. Sci. U.S.A. 88:6117-6121(1991).
DR PIR; A41117; A41117.
DR GO; GO:0003990; F:acetylcholinesterase activity; IEA.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 918 MW; 7F576453769B1DD8 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SELW 9
Db 2 AEMW 5

RESULT 15
Q9TR47
ID Q9TR47 PRELIMINARY; PRT; 10 AA.
AC Q9TR47;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Amphoterin homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;
RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
RA Nagashima M., Lundh E.R., Vijay S., Nitecki D.;
RT "The receptor for advanced glycation end products (RAGE) is a cellular
RT binding site for amphoterin. Mediation of neurite outgrowth and CO-
RT expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761(1995).
SQ SEQUENCE 10 AA; 1163 MW; 28E5034453769B18 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ELWTS 11
Db 4 EWMW 8

Search completed: April 27, 2005, 15:29:49
Job time : 176 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	34	56.7	8	3	ADB09130		Aab09130 Hepatitis
2	31	51.7	10	8	ADK09671		Adk09671 Human pap
3	31	51.7	10	8	ADK09188		Adk09188 Human pap
4	30	50.0	6	6	ABR46515		AbR46515 Staphyloc
5	30	50.0	9	2	AAR72493		Aar72493 Dengue vi
6	30	50.0	10	2	AAW37198		Aaw37198 Human onc
7	29	48.3	7	2	AAV33139		Aav33139 Rabbit ca
8	29	48.3	10	5	AAU93215		Aau93215 Granulocy
9	29	48.3	11	6	ABJ37125		Abj37125 Rhodopsin
10	28	46.7	6	6	ABR46459		AbR46459 Staphyloc
11	28	46.7	7	8	ADJ68302		Adj68302 Androgen
12	28	46.7	9	2	AYO04678		Ayo04678 Peptide #
13	28	46.7	10	4	ABE55959		AbE55959 Vascular
14	28	46.7	11	3	AAV93379		Aav93379 Binding m
15	28	46.7	11	7	ADF53467		AdF53467 MCPC 603
16	27	45.0	6	2	AAR89913		Aar89913 p53/MDM2
17	27	45.0	6	2	AAW13606		Aaw13606 p53 prote
18	27	45.0	6	3	AAE17074		Aae17074 Mdm/hdm a
19	27	45.0	6	5	ABB73169		Abb73169 Mdm/hdm a
20	27	45.0	6	6	ABR46627		AbR46627 Staphyloc
21	27	45.0	6	6	ABR46507		AbR46507 Staphyloc
22	27	45.0	6	6	ABG73432		Abg73432 Human p53
23	27	45.0	6	7	ADJ73323		Adj73323 Mdm/hdm a
24	27	45.0	6	8	ADJ52957		Adj52957 CH1 delet
25	27	45.0	6	8	ADJ51918		Adj51918 CH1 delet

CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and
 CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 8 AA;

Query Match 56.7%; Score 34; DB 3; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 FSELWTS 11
 |||||
 Db 1 FSHLWTS 7

RESULT 2
 ADK09671
 ID ADK09671 standard; peptide; 10 AA.

XX AC ADK09671;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus peptide #1726.

KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.

OS Human papillomavirus.

PN WO2004011650-A2.

PD 05-FEB-2004.

PF 24-JUL-2003; 2003WO-EP008112.

PR 24-JUL-2002; 2002AT-00001124.

PR 11-JUL-2003; 2003EP-00450171.

PA (INTE-) INTERCELL AG.

PI Mattner F, Schmidt W, Habel A;

PS WPI; 2004-169243/16.

PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.

PS Claim 18; Page 192; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.

SQ Sequence 10 AA;

Query Match 51.7%; Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 96;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SPFSRLWT 10

Db |||||
 1 SPFSRTWS 8

RESULT 3

ADK09188
 ID ADK09188 standard; peptide; 10 AA.

XX AC ADK09188;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus peptide #1243.

KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.

OS Human papillomavirus.

PN WO2004011650-A2.

PD 05-FEB-2004.

PF 24-JUL-2003; 2003WO-EP008112.

PR 24-JUL-2002; 2002AT-00001124.

PR 11-JUL-2003; 2003EP-00450171.

PA (INTE-) INTERCELL AG.

PI Mattner F, Schmidt W, Habel A;

PS WPI; 2004-169243/16.

PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.

PS Claim 18; Page 187; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.

SQ Sequence 10 AA;

Query Match 51.7%; Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 96;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SPFSRLWT 10
 |||||
 Db 1 SPFSRTWS 8

RESULT 4

ABR46515
 ID ABR46515 standard; peptide; 6 AA.

XX AC ABR46515;

DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #1705.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 PN 23-JAN-2003.
 PD 11-JUL-2001; 2001WO-EP008004.
 PF 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 PR (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 DR Combination of peptides derived from chemotaxis inhibiting protein from
 XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 17; 89pp; English.
 PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 XX -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ Query Match 50.0%; Score 30; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 FFEELW 9
 Db 1 FFEELW 6
 RESULT 5
 AAW72493
 ID AAW72493 standard; peptide; 9 AA.
 XX AAW72493;
 AC 23-DEC-1998 (first entry)
 DT Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #38.
 XX Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;
 KW dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;
 KW immunisation; immunoreactive; infection.
 XX Dengue virus.
 OS US5824506-A.
 PN 20-OCT-1998.
 PD

XX 15-AUG-1994; 94US-00290268.
 XX 15-AUG-1994; 94US-00290268.
 PR (GENE-) GENELABS DIAGNOSTICS PTE LTD.
 XX Chan L, Guan M;
 PI WPI; 1998-582552/49.
 DR Dengue virus peptide antigens - especially for diagnosis of dengue virus
 PT infection.
 PT Example 1; Col 17; 21pp; English.
 XX AAW72456 to AAW72570 represent peptide fragments from the dengue virus
 CC type-2 glycoprotein NS1, which was used in an example from the present
 CC invention for an epitope mapping assay. The invention has developed
 CC peptide antigens consisting of fragments of the dengue virus NS1 protein.
 CC The peptide antigens can be used for the diagnosis of dengue virus
 CC infection by detection of antibodies to the virus, especially in an assay
 CC comprising attaching the antigen to a solid support, contacting a serum
 CC sample with the support, and detecting bound antibodies with a labelled
 CC anti-human antibody or used for preparing vaccines against dengue virus
 CC infection
 XX Sequence 9 AA;
 SQ Query Match 50.0%; Score 30; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GSFFSELM 9
 Db 1 GVFFINIW 8
 RESULT 6
 AAW37198
 ID AAW37198 standard; peptide; 10 AA.
 XX AAW37198;
 AC 20-JUL-1998 (first entry)
 DT Human oncogenic protein MDM2 binding Cys (Acrld) peptide derivative 2.
 XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumour; diagnosis; binding; viral infection.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; Sulphhydryl side-chain linked
 FT to 6-acryloyl-2-(dimethylamino) naphthalene"
 FT Modified-site 10
 FT /note= "C-terminal amide"
 FT WO9801467-A2.
 PN 15-JAN-1998.
 PD 04-JUL-1997; 97WO-EP003549.
 XX 05-JUL-1996; 96GB-00014197.
 PR 07-APR-1997; 97GB-00007041.
 XX (NOVS) NOVARTIS AG.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX

PI Lane D, Boettger V, Boettger A, Pickley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX Compounds binding to MDW2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX Example 2; Page 20; 45pp; English.
XX This is a Cys (Acrld) peptide derivative capable of binding to a human
CC onco-genic protein MDW2. The MDW2 binding peptides can specifically
CC inhibit or block the binding of MDW2 to the human p53 protein, in vitro
CC or in vivo. Inhibiting the interaction between the p53 and MDW2 can
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC p53 and non-elevated levels of MDW2. The peptides may be used to identify
CC molecules that bind to MDW2 and to identify and design inhibitors of
CC MDW2/p53 binding. They may also be used to purify binding partners
CC especially MDW2, diagnose disease by measuring levels of MDW2 in blood of
CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDW2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDW2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDW2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX Sequence 10 AA;
SQ Query Match 50.0%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2;
QY 2 GSFFSELW 9
Db 2 GTFESDLW 9
RESULT 7
AAV33139
ID AAY33139 standard; peptide; 7 AA.
XX AAY33139;
XX 16-NOV-1999 (first entry)
XX Rabbit carboxylesterase protein fragment #3.
XX Carboxylesterase; rabbit; tumour cell; chemotherapy; prodrug;
XX disease-specific responsive promoter; CRT-11; APC; resection; recurrence;
XX inhibition; bone marrow cell.
XX Oryctolagus cuniculus.
XX WO9942593-A1.
XX 26-AUG-1999.
XX 12-FEB-1999; 99WO-US003171.
XX 19-FEB-1998; 98US-0075258P.
XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX Danks MK, Potter PM, Houghton PJ;
XX WPI; 1999-540311/45.
XX New carboxylesterase polypeptide for treatment of tumors.
XX Example 2; Page 57; 70pp; English.
CC This invention describes a novel rabbit carboxylesterase polypeptide (I)
CC capable of metabolizing a chemotherapeutic prodrug and its inactive
CC metabolites into an active drug. The invention also describes a
CC composition comprising (I) and a disease-specific responsive promoter.
CC This composition is useful for sensitizing tumor cells to a
CC chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into
CC tumor cells, and contacting the sensitized cells with a chemotherapeutic
CC prodrug to inhibit growth of the tumor cells. The composition can also be
CC administered to the site of tumor resection to inhibit tumor recurrence,
CC and be administered to bone marrow cells to remove tumor cells. The
CC products of the invention are useful for identifying drugs that are
CC inactivated by a carboxylesterase enzyme, and are also useful for
CC identifying compounds containing a COOC ester linkage that are activated
CC by a carboxylesterase enzyme. This sequence represents a fragment of a
CC rabbit carboxylesterase which is described in the method of the invention
XX Sequence 7 AA;
SQ Query Match 48.3%; Score 29; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 SFFSELW 9
Db 1 AFWTEWLW 7
RESULT 8
AAU93215
ID AAU93215 standard; peptide; 10 AA.
XX AAU93215;
XX 02-JUL-2002 (first entry)
XX Granulocyte-colony stimulating factor receptor binding peptide #21.
XX G-CSFR; granulocyte-colony stimulating factor receptor; cytokine;
XX haematopoietic growth factor; neutrophil proliferation; AIDS;
XX neutrophil differentiation; acquired immunodeficiency syndrome;
XX chemotherapy-induced neutropenia; community acquired pneumonia;
XX depressed neutrophil count; immunostimulant.
XX Synthetic.
XX WO200207676-A2.
XX 31-JAN-2002.
XX 20-JUL-2001; 2001WO-US023046.
XX 20-JUL-2000; 2000US-00620091.
XX (GLAX) GLAXO GROUP LTD.
XX Cwiria SE, Balu P, Duffin DJ, Piplani S, Meeowen-Merrill B;
XX Schatz PJ;
XX WPI; 2002-329382/36.
XX Novel compounds, useful for treating depressed neutrophil count, comprise
XX peptide chains of approximately 6 to 40 amino acids in length that bind
XX to granulocyte-colony stimulating factor receptor.
XX Claim 3; Page 52; 90pp; English.
XX The invention relates to compounds comprising a peptide chain
XX approximately 6 to 40 amino acids in length that binds to granulocyte-
XX colony stimulating factor receptor (G-CSFR). The compounds contain
XX specific sequences of the generic peptides appearing as AAU79402-AAU79406
XX and the generic sequences XV 1XV 2XV 3XV 4XV 5XV 6XV 7XV 8 (where XV_1 =
XX E, C, Q, V or Y; XV_2 = E, A, L, M, S, W or Q; XV_3 = K, R or T; XV_4 =
XX L, A or V; XV_5 = R, A, M, H, E, V, L, G, D, Q or S; XV_6 = E or V; XV_7

CC = A or G; and XV_8 = R, H, G or L) and XVI_1XVI_2XVI_3XVI_4XVI_5
 CC EXVI_6XVI_7XVI_8XVI_9 (where XVI_1 = A, E or G; XVI_2 = E, H or D; XVI_3
 CC = R or G; XVI_4 = K, Y, M, N, Q, R, D, I, S or E; XVI_5 = A, S or P;
 CC XVI_6 = E, D, T, Q, K or R; XVI_7 = R, W, K, L, S, A or Q; XVI_8 = R or E
 CC ; and XVI_9 = W, G or R). The compounds are used for treating conditions
 CC associated with depressed neutrophil count e.g. chemotherapy-induced
 CC neutropenia, AIDS-induced neutropenia or community-acquired pneumonia-
 CC induced pneumonia. The compounds are useful as in vitro as tools for
 CC understanding the biological role of granulocyte-colony stimulating
 CC factor (G-CSF) a haematopoietic growth factor and cytokine that stimulates
 CC neutrophil proliferation and differentiation), including evaluation of
 CC many factors thought to influence, and be influenced by, production of
 CC white blood cells, in the development of compounds that bind to G-CSFR,
 CC as reagents for detecting G-CSF receptor or related receptor on living
 CC cells, fixed cells, in biological fluid, in tissue homogenates or in
 CC purified natural biological materials, in situ staining, fluorescence-
 CC activated cell sorting (FACS), Western blotting or enzyme-linked
 CC immunoadsorbent assay (ELISA), in receptor purification or in purifying
 CC cells expressing G-CSFR on the cell surface (or inside permeabilised
 CC cells) as a commercial research reagent for various medical and
 CC diagnostic uses or to treat a disease that would benefit from the ability
 CC to of a compound to mimic the effects of G-CSF in vivo. The compounds
 CC bind specifically to G-CSFR and allow for studies of biological
 CC activities mediated by the receptor and for the treatment of diseases,
 CC disorders and conditions that would benefit from activating or
 CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
 CC the invention
 CC
 CC Sequence 10 AA;
 CC

Query Match 48.3%; Score 29; DB 5; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPFSELW 9
 ||: |||
 Db 3 SPWVELW 9

RESULT 9
 ABJ37125
 ID ABJ37125 standard; peptide; 11 AA.

AC ABJ37125;

XX 08-MAY-2003 (first entry)

XX Rhodopsin related G-protein coupled receptor binding site peptide #1.
 DE Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
 XX Rhodopsin.

XX Unidentified.

XX WO2003004147-A2.

XX 16-JAN-2003.

XX 05-JUL-2002; 2002WO-GB003094.

XX 06-JUL-2001; 2001GB-00016570.

XX (BIOF-) BIOFOCUS PLC.

XX Crossley R, Rose VS, Stevens AP;

XX WPI; 2003-221549/21.

XX Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting with
 PT ligand and motifs interacting with microenvironment, and assembling
 PT motifs.

PS Disclosure; Fig 1; 39pp; English.

XX The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for synthesis. The
 CC novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,
 CC which relates to the novel compound library production method of the
 CC invention

XX Sequence 11 AA;

Query Match 48.3%; Score 29; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ELWTS 11
 |||||
 Db 2 ELWTS 6

RESULT 10

ABR46459

ID ABR46459 standard; peptide; 6 AA.

AC ABR46459;

XX 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #1649.

DE CHIPS; Chemotaxis Inhibitory Protein; CSA-receptor; CSaR;
 KW formylated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; anti-inflammatory;
 KW candidant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.

OS Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

XX Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.

PS Disclosure; Page 16; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5ar) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match 46.7%; Score 28; DB 6; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches: 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PFSELM 9
 |||:|
 Db 1 PFFEIW 6

RESULT 11
 ADR68302
 ID ADR68302 standard; peptide; 7 AA.

XX ADR68302;

DT 02-DEC-2004 (first entry)

XX Androgen receptor interacting peptide SEQ ID NO:20.

DE androgen receptor binding peptide; androgen receptor interacting peptide;
 XX androgen receptor; cytostatic; gene therapy; prostate cancer.

XX Mammalia.
 OS Synthetic.

XX WO2004076473-A2.

XX 10-SEP-2004.

XX 10-FEB-2004; 2004WO-US003774.

XX 12-FEB-2003; 2003US-0446955P.

XX (KARO-) KARO BIO AB.

XX Buehrer BM, Barnett TR;

XX WPI; 2004-653365/63.

XX New polypeptides that bind to the androgen receptor, useful for
 PT diagnosing or treating diseases associated with abnormal levels of
 PT activation of androgen receptor, e.g. prostate cancer, or in biological
 PT research.

PS Disclosure; SEQ ID NO 20; 46pp; English.

XX The present invention describes a polypeptide that binds to the androgen
 CC receptor, or a polypeptide that comprises at least 50% amino acid
 CC sequence identity to the polypeptide. Also described: (1) methods of
 CC analysing the surface conformation of a protein using one or more of the
 CC polypeptide sequences mentioned above; (2) methods of identifying
 CC modulators of protein function using one or more of the polypeptide
 CC sequences mentioned above; (3) a pharmaceutical composition comprising a
 CC pharmaceutical carrier and one or more of the polypeptide sequences
 CC described above; (4) a peptide that binds to the androgen receptor, the
 CC binding being competitively inhibited by the polypeptide described above;
 CC (5) a chimeric protein comprising the above polypeptide and at least a
 CC portion of a filamentous phage protein, the portion of the filamentous
 CC phage protein being sufficient for integration of the chimeric protein
 CC into the coat of phage particles to display the polypeptide; (6) a
 CC filamentous phage displaying the above polypeptide; (7) a method of
 CC diagnosing a disease in a patient characterised by abnormal levels of
 CC activation of androgen receptor, comprising providing a sample of body

CC fluid or tissue of the patient, administering a diagnostic amount of the
 CC pharmaceutical composition described above, and assaying the amount of
 CC activated androgen receptor in the body fluid or tissue of the patient;
 CC and (8) a method of treating a patient suffering from a disease
 CC characterised by abnormal levels of activation of androgen receptor,
 CC comprising administering to the patient a therapeutic amount of the
 CC pharmaceutical composition described above. The androgen receptor
 CC interacting polypeptide has cytostatic activity, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing or
 CC treating patients suffering from diseases characterised by abnormal
 CC levels of activation of androgen receptor, such as prostate cancer. They
 CC may also be used in biological research, as therapeutics or for in vitro
 CC or in vivo classification of compounds. The present sequence represents
 CC an androgen receptor interacting peptide, which is used in the
 CC exemplification of the present invention.

XX Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SFFSELM 9
 |||:|
 Db 1 SRFAELW 7

RESULT 12

AAAY04678

ID AAY04678 standard; peptide; 9 AA.

XX AAY04678;

XX 22-JUN-1999 (first entry)

XX Peptide #13 encoded by HsdR/M/S gene fragment.

DE HsdR; HsdM; HsdS; restriction/modification; bacteriophage; resistance;
 KW lactic acid bacterium.

XX Lactococcus lactis.

XX FR2767831-A1.

XX 05-MAR-1999.

XX 02-SEP-1997; 97FR-00010885.

XX 02-SEP-1997; 97FR-00010885.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Chopin MC, Clier F, Ehrlich SD, Gautier M, Schouler C;

XX WPI; 1999-183265/16.

XX Bacteriophage resistance mechanism subunit polypeptides - of lactic acid
 PT bacteria, especially Lactobacillus lactis.

XX Claim 7; Page 62; 65pp; French.

PS The invention relates to polypeptides that constitute the HsdR, HsdM or
 CC HsdS subunit of a R/M [restriction/modification] type IC bacteriophage
 CC resistance mechanism active against the phages of lactic acid bacteria,
 CC especially Lactococcus lactis. Also claimed are fragments of the HsdR,
 CC HsdM and HsdS gene which encode peptides AA104666-Y04679. Nucleic acids
 CC encoding the HsdR, HsdM or HsdS fragment can be used for expression of at
 CC least one bacteriophage resistance mechanism in a lactic acid bacterium

XX Sequence 9 AA;

Query Match 46.7%; Score 28; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSFFSEL 8
 DB 2 GSFFKQL 8

RESULT 13
 ABB55959
 ID ABB55959 standard; peptide; 10 AA.
 XX AC ABB55959;
 XX DT 15-FEB-2002 (first entry)
 XX DE Vascular dementia-associated protein isoform (VPI) 159.
 XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 XX KW diagnosis; prognosis; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200169261-A2.
 XX PD 20-SEP-2001.
 XX PF 14-MAR-2001; 2001WO-GB001106.
 XX PR 15-MAR-2000; 2000GB-00006285.
 XX PR 24-NOV-2000; 2000GB-00028734.
 XX PR 28-NOV-2000; 2000US-00724391.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMC, Parekh RB, Rohlf C;
 XX DR WPI; 2001-557937/62.
 XX PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 XX PT determining stage of VD and monitoring the effect of VD therapy.
 XX PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 XX PT features correlated with VD.
 XX PS Claim 6; Page 33; 151pp; English.
 XX CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55901-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy

Sequence 10 AA;
 Query Match 46.7%; Score 28; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SFFSELW 9
 DB 1 SFFPENW 7

RESULT 14
 AAY93379

ID AAY93379 standard; peptide; 11 AA.
 XX AC AAY93379;
 XX DT 04-SEP-2000 (first entry)
 XX DE Binding moiety for a human parvovirus B19 polypeptide.
 XX KW Binding moiety; human parvovirus; B19 polypeptide; VPI capsid protein;
 XX KW VP2 capsid protein; blood; vaccine.
 XX OS Synthetic.
 XX PN WO200025807-A1.
 XX PD 11-MAY-2000.
 XX PF 04-NOV-1999; 99WO-US026275.
 XX PR 05-NOV-1998; 98US-00186958.
 XX PA (DYAX-) DYAX CORP.
 XX PI Whelihan EF;
 XX DR WPI; 2000-365396/31.
 XX PT Human parvovirus B19 polypeptide binding moiety, used to detect, clear
 XX PT and isolate parvovirus B19 polypeptides from blood and other solutions.
 XX PS Claim 2; Page 36; 47pp; English.
 XX CC AAY93377-94 represent binding moieties for human parvovirus B19 or B19-
 CC like polypeptides, particularly VPI or VP2 capsid proteins. AAY93377-85
 CC are isolated from a TN7 library, AAY93386-89 are isolated from a TN8
 CC library, and AAY93390-94 are isolated from a TN9 library. The B19 binding
 CC moieties can be used for detection and clearing of parvovirus B19 and/or
 CC B19-like polypeptides from any solution which contains them, e.g. blood.
 CC They may also be used to isolate parvovirus B19 and/or B19-like viruses
 CC or polypeptides, which may be used in parvovirus vaccines
 XX SQ Sequence 11 AA;
 Query Match 46.7%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 FSELWTS 11
 DB 1 FFCALWPS 8

RESULT 15
 ADF53467
 ID ADF53467 standard; peptide; 11 AA.
 XX AC ADF53467;
 XX DT 12-FEB-2004 (first entry)
 XX DE MCP6 603 antibody CDR3 mutant peptide amino acid sequence 10.
 XX KW walk-through mutagenesis; prototype amino acid; prototype nucleotide;
 XX KW mutant polypeptide production; MCP6 603;
 XX KW complementarity determining region; CDR; heavy chain; CDR3; mutant;
 XX KW mutin.
 XX OS Unidentified.
 XX OS Synthetic.
 XX PN WO20003089671-A1.
 XX PD 30-OCT-2003.

```

XX PF 16-APR-2003; 2003WO-US011935.
XX PR 17-APR-2002; 2002US-0373686P.
XX PA (CREA/) CREA R.
XX PA (CAPP/) CAPPUCILLI G.
XX PI Crea R, Cappuccilli G;
XX DR WPI; 2003-854132/79.
XX PT Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
PT for producing mutant polypeptides comprising synthesizing oligonucleotides
PT comprising a nucleotide sequence for each target region of a prototype
PT amino acid.
XX PS Example; Fig 7; 40pp; English.
XX CC This invention relates to a novel method of walk-through mutagenesis of a
CC nucleic acid encoding a polypeptide which comprises synthesising a
CC mixture of oligonucleotides comprising a nucleotide sequence for each
CC target region of a prototype amino acid, where each oligonucleotide
CC contains, at each sequence position in the target region, a prototype
CC nucleotide for synthesis of the prototype amino acid or a predetermined
CC nucleotide that is required for synthesis of the predetermined amino
CC acid. The method is useful in producing mutant polypeptides in which the
CC overall presence of the predetermined amino acid is limited to one or two
CC positions per mutated polypeptide, leaving the remaining amino acids in
CC the targeted region intact or as close as possible to the prototype
CC sequence. The invention was exemplified using the three complementarity
CC determining regions (CDRs) of the heavy chain of the monoclonal antibody
CC MCPC 603.
XX SQ Sequence 11 AA;
XX
XX Query Match 46.7%; Score 28; DB 7; Length 11;
XX Best Local Similarity 44.4%; Pred. No. 3.6e+02;
XX Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 SPFFSELWTS 11
XX |::| |::|
XX Db 1 SYSSSSWS 9
XX
XX Search completed: April 27, 2005, 15:26:49
XX Job time : 172 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:23:03 ; Search time 42 Seconds
(without alignments)
19.551 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFSELMWS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	56.7	8	4	US-08-469-260A-252
2	34	56.7	8	4	US-08-488-446-252
3	34	56.7	8	4	US-08-467-344A-252
4	34	56.7	8	4	US-08-424-550B-252
5	30	50.0	6	1	US-08-424-957-6
6	30	50.0	6	3	US-09-035-686-6
7	30	50.0	11	1	US-08-424-957-42
8	30	50.0	11	3	US-09-035-686-42
9	29	48.3	7	4	US-09-595-682B-10
10	29	48.3	10	4	US-09-620-091-28
11	28	46.7	11	3	US-09-186-958-6
12	28	46.7	11	3	US-09-669-271A-6
13	28	46.7	11	4	US-09-881-276-6
14	27	45.0	6	1	US-08-424-957-2
15	27	45.0	6	3	US-09-035-686-2
16	27	45.0	6	3	US-09-081-975-1
17	27	45.0	6	4	US-09-428-082B-130
18	27	45.0	6	4	US-09-732-384-4
19	27	45.0	7	1	US-08-277-660A-27
20	27	45.0	7	1	US-08-424-957-15
21	27	45.0	7	1	US-08-424-957-19
22	27	45.0	7	3	US-09-035-686-15
23	27	45.0	7	3	US-09-035-686-19
24	27	45.0	7	3	US-09-035-686-15
25	27	45.0	10	1	US-08-277-660A-7
26	27	45.0	10	1	US-08-424-957-11
27	27	45.0	10	1	US-08-424-957-18

28	27	45.0	10	3	US-09-035-686-11	Sequence 11, Appl
29	27	45.0	10	3	US-09-035-686-18	Sequence 18, Appl
30	27	45.0	11	1	US-08-277-660A-9	Sequence 9, Appl
31	27	45.0	11	1	US-08-277-660A-10	Sequence 10, Appl
32	27	45.0	11	1	US-08-277-660A-11	Sequence 11, Appl
33	27	45.0	11	1	US-08-277-660A-12	Sequence 12, Appl
34	27	45.0	11	1	US-08-277-660A-13	Sequence 13, Appl
35	27	45.0	11	1	US-08-277-660A-19	Sequence 19, Appl
36	27	45.0	11	1	US-08-277-660A-20	Sequence 20, Appl
37	27	45.0	11	1	US-08-424-957-17	Sequence 17, Appl
38	27	45.0	11	1	US-08-424-957-23	Sequence 23, Appl
39	27	45.0	11	1	US-08-424-957-24	Sequence 24, Appl
40	27	45.0	11	1	US-08-424-957-25	Sequence 25, Appl
41	27	45.0	11	1	US-08-424-957-26	Sequence 26, Appl
42	27	45.0	11	1	US-08-424-957-32	Sequence 32, Appl
43	27	45.0	11	1	US-08-424-957-33	Sequence 33, Appl
44	27	45.0	11	1	US-08-424-957-34	Sequence 34, Appl
45	27	45.0	11	1	US-08-424-957-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-469-260A-252

Query Match 56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 FSELWTS 11
|||
Db 1 FSHLWTS 7

RESULT 2

US-08-488-446-252
; Sequence 252, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/488,446
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 FSELWTS 11
|||
Db 1 FSHLWTS 7

RESULT 3

US-08-467-344A-252

; Sequence 252, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Query Match 56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 FSELWTS 11
|||
Db 1 FSHLWTS 7

RESULT 4

US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Patent No. 6720166
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF

APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POROMBESKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FSELWTS 11
Db 1 FSHLWTS 7

RESULT 5
US-08-424-957-6
; Sequence 6, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WH/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-6

Query Match 50.0%; Score 30; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9
Db 2 FSELW 6

RESULT 6
US-09-035-686-6
; Sequence 6, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-6

Query Match 50.0%; Score 30; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
 Db 2 FSELM 6

RESULT 7
 US-08-424-957-42
 ; Sequence 42, Application US/08424957
 ; Patent No. 5770377
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickaley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,957

; FILING DATE: 19-APR-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/277,660

; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WH
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-424-957-42

Query Match 50.0%; Score 30; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
 Db 5 FSELM 9

RESULT 8
 US-09-035-686-42
 ; Sequence 42, Application US/09035686
 ; Patent No. 6153391
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickaley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/035,686
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/424,957

; FILING DATE: 19-APR-1995
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WH
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-09-035-686-42

Query Match 50.0%; Score 30; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
 Db 5 FSELM 9

RESULT 9
 US-09-595-682B-10
 ; Sequence 10, Application US/09595682B
 ; Patent No. 6800483
 ; GENERAL INFORMATION:
 ; APPLICANT: Danks, Mary K.
 ; APPLICANT: Potter, Philip M.
 ; APPLICANT: Houghton, Peter J.
 ; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
 ; TITLE OF INVENTION: Tumor Cells
 ; FILE REFERENCE: SJ-0005
 ; CURRENT APPLICATION NUMBER: US/09/595,682B
 ; CURRENT FILING DATE: 2000-01-16
 ; PRIOR APPLICATION NUMBER: 60/075,258
 ; PRIOR FILING DATE: 1998-02-19
 ; PRIOR APPLICATION NUMBER: PCT/US99/03171
 ; PRIOR FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-09-595-682B-10

Query Match 48.3%; Score 29; DB 4; Length 7;

Best Local Similarity 57.1%; Pred. No. 4.1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 3;

Qy 3 SPFGSLW 9
|:|:|:|
Db 1 AFWTELM 7

RESULT 10

US-09-620-091-28
; Sequence 28, Application US/09620091
; Patent No. 6716811
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; TITLE OF INVENTION: USES
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/09/620,091
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-620-091-28

Query Match 48.3%; Score 29; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPFGSLW 9
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Db 3 SPFWELW 9

RESULT 11

US-09-186-958-6
; Sequence 6, Application US/09186958B
; Patent No. 6238860
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Payelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/186,958B
; CURRENT FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
US-09-186-958-6

Query Match 46.7%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FFSLEWTS 11
|:|:|:|
Db 1 PFCALWPS 8

RESULT 12

US-09-669-271A-6
; Sequence 6, Application US/09669271A
; Patent No. 6291197
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Payelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/669,271A
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
US-09-669-271A-6

Query Match 46.7%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FFSLEWTS 11
|:|:|:|
Db 1 PFCALWPS 8

RESULT 13

US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. 6479641
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Payelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
US-09-881-276-6

Query Match 46.7%; Score 28; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FFSLEWTS 11
|:|:|:|
Db 1 PFCALWPS 8

RESULT 14

US-08-277-660A-2
; Sequence 2, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.

APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,660A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-60244/WHd
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-277-660A-2

Query Match 45.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSELW 9
||:|
Db 2 FSDLW 6

RESULT 15
US-08-424-957-2
Sequence 2, Application US/08424957
Patent No. 5770377
GENERAL INFORMATION:
APPLICANT: Pickaley, Steven M.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660

FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHd
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-2
Query Match 45.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 5 FSELW 9
||:|
Db 2 FSDLW 6

Search completed: April 27, 2005, 15:31:20
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:29:56 ; Search time 130 Seconds
(without alignments)
28.159 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFSELMWTS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 197300

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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3: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US10H_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	56.7	8	US-08-424-550B-252	Sequence 252, App
2	30	50.0	10	US-09-214-371-35	Sequence 35, Appl
3	30	50.0	10	US-09-214-371-36	Sequence 36, Appl
4	29	48.3	10	US-10-659-207-28	Sequence 28, Appl
5	28	46.7	9	US-09-486-734A-35	Sequence 35, Appl
6	28	46.7	11	US-09-881-276-6	Sequence 6, Appl
7	28	46.7	11	US-10-417-895A-56	Sequence 56, Appl
8	27	45.0	6	US-09-214-371-83	Sequence 83, Appl
9	27	45.0	6	US-09-732-384-4	Sequence 4, Appl
10	27	45.0	6	US-10-155-059-1	Sequence 1, Appl
11	27	45.0	6	US-10-609-217-130	Sequence 130, App
12	27	45.0	6	US-10-632-388-130	Sequence 130, App
13	27	45.0	6	US-10-651-723-130	Sequence 130, App

14	27	45.0	6	15	US-10-645-761-130	Sequence 130, App
15	27	45.0	6	15	US-10-666-696-130	Sequence 130, App
16	27	45.0	6	15	US-10-653-048-130	Sequence 130, App
17	27	45.0	8	16	US-10-340-179-2	Sequence 2, Appl
18	27	45.0	8	16	US-10-340-179-3	Sequence 3, Appl
19	27	45.0	9	9	US-09-214-371-37	Sequence 37, Appl
20	27	45.0	9	9	US-09-214-371-38	Sequence 38, Appl
21	27	45.0	9	16	US-10-340-179-1	Sequence 1, Appl
22	27	45.0	10	17	US-10-726-332-107	Sequence 107, App
23	27	45.0	11	10	US-09-840-085-31	Sequence 31, Appl
24	26	43.3	8	15	US-10-387-957-36	Sequence 36, Appl
25	26	43.3	8	15	US-10-387-957-37	Sequence 37, Appl
26	26	43.3	8	15	US-10-387-957-38	Sequence 38, Appl
27	26	43.3	8	15	US-10-387-957-39	Sequence 39, Appl
28	26	43.3	8	15	US-10-387-934-36	Sequence 36, Appl
29	26	43.3	8	15	US-10-387-934-37	Sequence 37, Appl
30	26	43.3	8	15	US-10-387-934-38	Sequence 38, Appl
31	26	43.3	8	15	US-10-387-934-39	Sequence 39, Appl
32	26	43.3	8	16	US-10-387-955-36	Sequence 36, Appl
33	26	43.3	8	16	US-10-387-955-37	Sequence 37, Appl
34	26	43.3	8	16	US-10-387-955-38	Sequence 38, Appl
35	26	43.3	8	16	US-10-387-955-39	Sequence 39, Appl
36	26	43.3	10	15	US-10-462-452-707	Sequence 707, App
37	26	43.3	10	15	US-10-601-953-812	Sequence 812, App
38	26	43.3	10	16	US-10-322-266-708	Sequence 708, App
39	25	41.7	8	17	US-10-480-954-233	Sequence 233, App
40	25	41.7	8	17	US-10-480-954-235	Sequence 235, App
41	25	41.7	8	17	US-10-480-954-237	Sequence 237, App
42	25	41.7	8	17	US-10-480-954-239	Sequence 239, App
43	25	41.7	9	14	US-10-014-340-245	Sequence 245, App
44	25	41.7	9	14	US-10-190-082-180	Sequence 180, App
45	25	41.7	9	15	US-10-239-656-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,508
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-424-550B-252

Query Match 56.7%; Score 34; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.3e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FSELWTS 11
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 Db 1 FSHLWTS 7

RESULT 2

US-09-214-371-35
 ; Sequence 35, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:

; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Pickseley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2

; FILE REFERENCE: 4-20937/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/214,371B
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549
 ; PRIOR FILING DATE: 1997-07-04
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 35

; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:peptide

; NAME/KEY: VARIANT

; LOCATION: (1)

; OTHER INFORMATION: X = Ac-Cys(Acrid)

; NAME/KEY: VARIANT

; LOCATION: (10)

; OTHER INFORMATION: X = Pro-NH2

; US-09-214-371-35

Query Match 50.0%; Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELW 9
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 Db 2 GPTFSDLW 9

RESULT 3

US-09-214-371-36

; Sequence 36, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:

; APPLICANT: Lane, David

; APPLICANT: Bottger, Volker

; APPLICANT: Bottger, Angelica
 ; APPLICANT: Pickseley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2

; FILE REFERENCE: 4-20937/A/PCT

; CURRENT APPLICATION NUMBER: US/09/214,371B

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: PCT/EP97/03549

; PRIOR FILING DATE: 1997-07-04

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:peptide

; NAME/KEY: VARIANT

; LOCATION: (1)

; OTHER INFORMATION: X = Ac-Cys

; NAME/KEY: VARIANT

; LOCATION: (10)

; OTHER INFORMATION: X = Pro-NH2

; US-09-214-371-36

Query Match 50.0%; Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELW 9
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 Db 2 GPTFSDLW 9

RESULT 4

US-10-659-207-28

; Sequence 28, Application US/10659207

; Publication No. US20050037959A1

; GENERAL INFORMATION:

; APPLICANT: CWIRLA, STEVEN E.

; APPLICANT: BALU, PALANI

; APPLICANT: DUFFIN, DAVID J.

; APPLICANT: PIPLANI, SUNILA

; APPLICANT: MERRILL, BARBARA MCEOWEN

; APPLICANT: SCHATZ, PETER JOSEPH

; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
 ; STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED

; TITLE OF INVENTION: USES

; FILE REFERENCE: 0300-0014

; CURRENT APPLICATION NUMBER: US/10/659,207

; CURRENT FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: US/09/620,091

; PRIOR FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 491

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

; US-10-659-207-28

Query Match 48.3%; Score 29; DB 17; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SFFSELW 9
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Db 3 SFWVWLW 9

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RESULT 5
; Sequence 35, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
; FILE REFERENCE: Bacteriophages of Lactic Acid Bacteria
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hads subunit
US-09-486-734A-35
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Query Match 46.7%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GSFFSEL 8
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Db 2 GSFFKQL 8

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RESULT 6
; Sequence 6, Application US/09881276
; Patent No. US20020031761A1
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Payelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polype
US-09-881-276-6
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Query Match 46.7%; Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 PFCALWPS 8

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RESULT 7
US-10-417-895A-56
; Sequence 56, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551-2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-56
```

Query Match 46.7%; Score 28; DB 15; Length 11;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SFFSELWTS 11
||| | :|
Db 1 SYSSSWSS 9

```
RESULT 8
US-09-214-371-83
; Sequence 83, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
; OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83
```

Query Match 45.0%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FSELW 9
||| | :|
Db 2 FSDLW 6

```
RESULT 9
US-09-732-384-4
; Sequence 4, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jidie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-4

Query Match      45.0%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 FSELM 9
Db      2 FSDLM 6

RESULT 10
US-10-155-059-1
; Sequence 1, Application US/10155059
; Publication No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
```

```
TELEFAX: 617-345-1300
TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-155-059-1

Query Match      45.0%; Score 27; DB 13; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 FSELM 9
Db      2 FSDLM 6

RESULT 11
US-10-609-217-130
; Sequence 130, Application US/10609217
; Publication No. US20040044189A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-130

Query Match      45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 FSELM 9
Db      2 FSDLM 6

RESULT 12
US-10-632-388-130
; Sequence 130, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
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; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-130

Query Match          45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELW 9
Db 2 FSDLW 6

RESULT 13
US-10-651-723-130
; Sequence 130, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-651-723-130

Query Match          45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELW 9
Db 2 FSDLW 6

RESULT 14
US-10-645-761-130
; Sequence 130, Application US/10645761
; Publication No. US2004007172A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-645-761-130

Query Match          45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELW 9
Db 2 FSDLW 6

RESULT 15
US-10-666-696-130
; Sequence 130, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mdm/hdm antagonist peptide
US-10-666-696-130

Query Match          45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELW 9
Db 2 FSDLW 6

Search completed: April 27, 2005, 15:42:33
Job time : 131 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:30:37 ; Search time 43 Seconds
(without alignments)
26.851 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFFSELWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	44.8	10	2	hypothetical prote
2	28	41.8	9	2	Ig heavy chain V r
3	25	37.3	12	2	Ig heavy chain CND
4	24	35.8	7	2	Ig H chain V-D-J r
5	22	32.8	9	2	T-cell receptor ga
6	20	29.9	6	2	dnaA protein - Pse
7	20	29.9	10	2	cytochrome-c oxida
8	20	29.9	11	2	corazonin - Americ
9	19	28.4	5	2	Leu-enkephalin - b
10	19	28.4	5	2	Met-enkephalin - b
11	19	28.4	6	2	T-cell receptor be
12	19	28.4	6	2	neuropeptide GNFR
13	19	28.4	7	2	Met-enkephalin-Arg
14	19	28.4	8	2	acetylcholinestera
15	19	28.4	10	2	beta-neoendorphin
16	19	28.4	11	2	Ig heavy chain CND
17	19	28.4	12	2	thyroglobulin - ra
18	18	26.9	9	2	litorin - Rohde's
19	18	26.9	10	2	T-cell receptor ga
20	18	26.9	10	2	neuropeptide Pec-H
21	18	26.9	11	1	probable trpEG lea
22	18	26.9	11	2	chaperonin 10 homo
23	18	26.9	11	2	probable substance
24	18	26.9	12	2	Ig heavy chain - m
25	18	26.9	12	2	gene rPLP-A protei
26	18	26.9	12	2	I57678
27	17.5	26.1	8	2	T-cell receptor be
28	17	25.4	7	2	leucokinin V - Mad
29	17	25.4	8	2	neuropeptide led-C

30	17	25.4	8	2	S08995	hypertrehalosemic
31	17	25.4	8	2	A49823	adipokinetic hormo
32	17	25.4	8	2	A43976	hypertrehalosemic
33	17	25.4	8	2	B43976	hypertrehalosemic
34	17	25.4	8	2	A05169	neuropeptide M-I -
35	17	25.4	10	2	A31571	hypertrehalosemic/
36	17	25.4	11	2	I60434	68kDa neurofilamen
37	17	25.4	12	2	I64829	gene HEXA protein
38	17	25.4	12	2	PH1189	T-cell receptor al
39	17	25.4	12	2	PH1180	T-cell receptor al
40	17	25.4	12	2	PH1183	T-cell receptor al
41	17	25.4	12	2	PH1188	T-cell receptor al
42	17	25.4	12	2	PH1172	T-cell receptor al
43	17	25.4	12	2	PH1175	T-cell receptor al
44	16	23.9	4	2	PT0661	T-cell receptor be
45	16	23.9	7	4	I55382	hypothetical pepti

ALIGNMENTS

RESULT 1

C39191

hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis

C:Species: Bacteroides fragilis

C:Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993

C:Accession: C39191

R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.

J. Bacteriol. 173, 176-183, 1991

A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra

A:Reference number: A39191; MUID:91100280; PMID:1846135

A:Accession: C39191

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-10 <SPE>

A:Cross-references: GB:M37699

Query Match 44.8%; Score 30; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FFSRLWTS 12

DB 2 YFSRPWTS 9

RESULT 2

S36850

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

C:Accession: S36850

R:Jacob, J.; Kalsoe, G.

submitted to the EMBL Data Library, July 1992

A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl

A:Reference number: S25024

A:Accession: S36850

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-9 <JAC>

A:Cross-references: EMBL:X67387; NID:G50113; PIDN:CAA47799.1; PID:e51594; PID:gl333871

C:Keywords: heterotetramer; immunoglobulin

Query Match 41.8%; Score 28; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFF 6

DB 4 DYGSYF 9

RESULT 3

PT0274

IG heavy chain CRD3 region (clone 3-109B) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0274
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0274
 A:Molecule type: DNA
 A:Residues: 1-12 <YAM>
 A:Experimental source: B lymphocyte
 A:Keywords: heterotetramer; immunoglobulin

Query Match 37.3%; Score 25; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FSELWTS 12
 : ||||
 Db 3 YSSWTS 9

RESULT 4

PH1602
 IG H chain V-D-J region (wild-type clone 313) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1602
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1602
 A:Molecule type: DNA
 A:Residues: 1-7 <LBV>
 A:Experimental source: bone marrow pre-B lymphocyte
 A:Keywords: immunoglobulin

Query Match 35.8%; Score 24; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SELWT 11
 : ||||
 Db 3 SSLWT 7

RESULT 5

G41946
 T-cell receptor gamma chain (2t.23) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: G41946
 R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol. 11, 5902-5909, 1991
 A>Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
 A:Reference number: A41946; MUID:92049316; PMID:1658619
 A:Accession: G41946
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-9 <WHE>
 C:Keywords: T-cell receptor

Query Match 32.8%; Score 22; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGSFES 7
 : ||||
 Db 2 YGSYS 7

RESULT 6

B34835
 dnaA protein - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 C:Accession: B34835
 R:Fee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A>Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
 A:Reference number: A34835; MUID:90160310; PMID:2106132
 A:Accession: B34835
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <YEE>
 A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
 C:Keywords: DNA binding

Query Match 29.9%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ELW 10
 : ||||
 Db 4 ELW 6

RESULT 7

TI3838
 cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
 C:Species: Mitochondrion Bipes biporus
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: TI3838
 R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A>Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A:Reference number: 217789; MUID:97153826; PMID:9000757
 A:Accession: TI3838
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <MAC>
 A:Cross-references: UNIPROT:P92576; EMBL:U71335; NID:g1753232; PID:g1753235; PIDN:AA8482
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: COL
 C:Keywords: mitochondrion; oxidoreductase

Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SFPS 7
 : ||||
 Db 6 SFPS 9

RESULT 8

S05002
 corazonin - American cockroach
 C:Species: Periplaneta americana (American cockroach)
 C>Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
 C:Accession: S05002
 R:Veestra, J.A.
 FEBS Lett. 250, 231-234, 1989
 A>Title: Isolation and structure of corazonin, a cardioactive peptide from the american
 A:Reference number: S05002; MUID:89325572; PMID:2753132
 A:Accession: S05002
 A:Molecule type: protein
 A:Residues: 1-11 <VEE>
 A:Cross-references: UNIPROT:P11496
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:11/Modified site: amidated carboxyl end (Asn) #status experimental

```

A;Residues: 1-6 <PDB>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match      28.4%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SELW 10
Db 2 SSLW 5
  |||
  |||

RESULT 12
A43129
neuropeptide GNFRFamide - tapeworm (Moniezia expansa)
C;Species: Moniezia expansa
C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
C;Accession: A43129
R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
A;Title: GNFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the
A;Reference number: A43129; MUID:93312289; PMID:8323531
A;Accession: A43129
A;Molecule type: protein
A;Residues: 1-6 <MAU>
A;Cross-references: UNIPROT:P41966
C;Keywords: amidated carboxyl end; neuropeptide
F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match      28.4%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSFF 6
Db 1 GNFF 4
  |||
  |||

RESULT 13
A60224
Met-enkephalin-Arg-Phe - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C;Accession: A60224
R;Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; W
J. Neurochem. 56, 1914-1920, 1991
A;Title: Isolation and characterization of opioid peptides from rabbit cerebell
A;Reference number: A60224; MUID:91225680; PMID:2027006
A;Accession: A60224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MAD>
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide

Query Match      28.4%; Score 19; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGSF 5
Db 1 YGGF 4
  |||
  |||

RESULT 14
A41117
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C;Species: Naja naja oxiana (Asian cobra), Oxya cobra)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41117
R;Krenkamp, H.J.; Weise, C.; Raba, R.; Aaviksoar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991

```

A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo d

A;Reference number: A4117; MUID:91296772; PMID:2068091

A;Accession: A4117

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <KRE>

A;Cross-references: UNIPROT:O7L227

C;Keywords: carboxylic ester hydrolase

Query Match 28.4%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 SELW 10

Db :|||

2 AEMW 5

RESULT 15

A60410

beta-neoendorphin / dynorphin precursor - guinea pig

N;Alternate names: alpha-neoendorphin; proenkephalin B precursor

C;Species: Cavia porcellus (guinea pig)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000

C;Accession: A60410

R;Murphy, R.; Turner, C.A.

Peptides 11, 65-68, 1990

A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.

A;Reference number: A60410; MUID:90259864; PMID:2342991

A;Accession: A60410

A;Molecule type: protein

A;Residues: 1-10 <MUR>

C;Superfamily: proenkephalin

C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGSF 5

Db :|||

1 YGGF 4

Search completed: April 27, 2005, 15:43:23

Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 15:31:27 ; Search time 174 Seconds
(without alignments)
35.316 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFFSELWTS 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	24	35.8	11	2 O77895	O77895 oreochromis
2	24	35.8	11	2 O77896	O77896 oreochromis
3	23	34.3	11	2 P83537	P83537 lactobacill
4	22	32.8	12	2 Q9TRT7	Q9TRT7 bos taurus
5	21	31.3	9	2 O95953	O95953 homo sapien
6	20	29.9	10	2 Q6LA62	Q6LA62 homo sapien
7	20	29.9	10	2 P92576	P92576 bipes bipor
8	20	29.9	11	1 CORZ PERAM	P11496 periplaneta
9	20	29.9	11	2 O77894	O77894 oreochromis
10	20	29.9	11	2 O77898	O77898 oreochromis
11	20	29.9	11	2 O65CG7	O65CG7 sinaloa tom
12	20	29.9	12	2 O46664	O46664 macropus ro
13	20	29.9	12	2 Q61331	Q61331 mus musculu
14	19	28.4	6	1 FARP MONEX	P41966 moniezia ex
15	19	28.4	8	2 Q99MN0	Q99MN0 mus musculu
16	19	28.4	8	2 Q7LZ27	Q7LZ27 naja oxiana
17	19	28.4	10	2 Q9TR47	Q9TR47 bos taurus
18	19	28.4	10	2 Q8SHC6	Q8SHC6 furcifer be
19	19	28.4	11	2 Q9UC46	Q9UC46 homo sapien
20	19	28.4	12	2 Q33579	Q33579 rhodobacter
21	19	28.4	12	2 Q63579	Q63579 rattus norv
22	18	26.9	8	2 Q68LF1	Q68LF1 myrmotherul
23	18	26.9	8	2 Q68LG3	Q68LG3 sakesphorus
24	18	26.9	9	1 L1TR PHYRO	P08946 phyllomedus
25	18	26.9	9	2 Q9H3Y3	Q9H3Y3 homo sapien
26	18	26.9	9	2 Q8H9Z1	Q8H9Z1 cyanophage
27	18	26.9	9	2 Q90350	Q90350 gb virus c/
28	18	26.9	10	1 AXHX LOCM1	P81626 locusta mig
29	18	26.9	10	2 Q7M465	Q7M465 platypleura
30	18	26.9	10	2 Q8SHB1	Q8SHB1 rhampoleon
31	18	26.9	10	2 Q8SHB4	Q8SHB4 furcifer ve

32 18 26.9 10 2 Q8SHB7
33 18 26.9 10 2 Q8SHC0
34 18 26.9 10 2 Q8SHC3
35 18 26.9 11 1 LPW THETH
36 18 26.9 11 1 TKNA SCYCA
37 18 26.9 11 2 Q9UELO
38 18 26.9 11 2 Q7MIH1
39 18 26.9 12 2 Q8Y04
40 18 26.9 12 2 Q89243
41 18 26.9 12 2 Q8UVW0
42 18 26.9 12 2 Q90XT0
43 18 26.9 12 2 Q90XT2
44 18 26.9 12 2 Q90XT5
45 18 26.9 12 2 Q90XU4

ALIGNMENTS

RESULT 1

O77895 PRELIMINARY; PRT; 11 AA.
AC O77895;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroides;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050005; AAC1344.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3P47C9EA772045A3 CRC64;

Query Match 35.8%; Score 24; DB 2; Length 11;
Best Local Similarity 50.0%; Fred.No. 2.7e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FFSELWTS 12
| : | : | :
| : | : | :
DB 3 FWSILWVA 10

RESULT 2

O77896 PRELIMINARY; PRT; 11 AA.
AC O77896;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroides;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci.";

RL Genet. 149:1527-1537(1998).
 DR EMBL; AF050006; AAC41345.1; -.

FT NON_TER 1
 SQ SEQUENCE 11 AA; 1399 MW; 3P47DB7A772685A3 CRC64;

Query Match 35.8%; Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 5 FFSSELM 10
 Db 3 FWSMLW 8

RESULT 3
 ID P83537 PRELIMINARY; PRT; 11 AA.

AC P83537;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DE Unknown protein from 2D-page (Fragment)

OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.

NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE, AND INDUCTION.

RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RI DOI=10.1002/1615-9861(200206)2:6<765: AID-PROT7653.0.CO;2-V;

RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 Lactobacillus sanfranciscensis.";

RT Proteomics 2:765-774(2002).
 RL -!- INDUCTION: By elevated hydrostatic pressure.

CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 protein is: 65 kDa.

FT NON_TER 1
 SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GSFFS 7
 Db 1 GSFFA 5

RESULT 4
 ID Q9TRT7 PRELIMINARY; PRT; 12 AA.

AC Q9TRT7;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE 15 kDa amyloid protein A homolog (Fragment).

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.

NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92132498; PubMed=1734497;
 RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;

RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils

RT of bovine kidney.";
 RL Scand. J. Immunol. 35:63-69(1992).

FT NON_TER 1
 SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AEB CRC64;

Query Match 32.8%; Score 22; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 6.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 SFFSELM 10
 Db 1 SFFXEXY 7

RESULT 5
 ID O95953 PRELIMINARY; PRT; 9 AA.

AC O95953;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DE Galactocerebrosidase (EC 3.2.1.46) (Fragment).

GN Name=GALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBSJ databases.

DR GO; GO:0004336; F:Galactosylceramidase activity; IEA.
 DR GO; GO:0016798; F:Hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

KW Glycosidase; Hydrolase.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2AADC2C699C8 CRC64;

Query Match 31.3%; Score 21; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.6e+06;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GSFFSELM 10
 Db 2 GFMVADLW 9

RESULT 6
 ID Q6LA62 PRELIMINARY; PRT; 10 AA.

AC Q6LA62;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Amiloride-sensitive epithelial sodium channel gamma subunit
 (Fragment).

GN Name=SCNN1G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=96421599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
 RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;

RT "Genomic organization and the 5' flanking region of the gamma subunit
 of the human amiloride-sensitive epithelial sodium channel.";

RL J. Biol. Chem. 271:26062-26066(1996).
 RN [2]
 RP SEQUENCE FROM N.A.


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RX MEDLINE=98316780; PubMed=9854208;
RA Ludwig M., Bolkenius U., Wicket L., Marynen P., Bidlingmaier F.;
RT "Structural organization of the gene encoding the alpha-subunit of the
RT human amiloride-sensitive epithelial sodium channel.";
RL Hum. Genet. 102:576-581(1998).
DR EMBL; Z92982; CAB07506.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1157 MW; DBAFF833733B05A2 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 SPFSLW 10
Db 1 SVVSEKW 7

RESULT 7
P92576 PRELIMINARY; PRT; 10 AA.
AC P92576;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COL;
OS Bipes biporus (Baja worm lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
OX NCBI_TaxID=52188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RT rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL; U71335; AAB48271.1; -.
DR PIR; T13838; T13838.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPFS 7
Db 6 SPFS 9

RESULT 8
CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11436;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Corazonin.

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OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from the
RT American cockroach.";
RL FEBS Lett. 250:231-234(1989).
CC -|- FUNCTION: Cardioactive peptide. Corazonin is probably involved in
CC the physiological regulation of the heart beat.
CC -|- SUBCELLULAR LOCATION: Secreted.
DR PIR; S05002; S05002.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RES 11 11 Asparagine amide.
SQ SEQUENCE 11 AA; 1387 MW; C7CFE32D6415AB46 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FSELWTS 12
Db 5 YSRGWTN 11

RESULT 9
O77894 PRELIMINARY; PRT; 11 AA.
AC O77894;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincel V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050004; AAC41343.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PFSELW 10
Db 3 FWSIVW 8

RESULT 10
O77898 PRELIMINARY; PRT; 11 AA.
ID O77898
AC O77898;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OC NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo B., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.,
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050008; AAC41347.1; --
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 FFSLEW 10
 Db 3 FWSIVW 8

RESULT 11
 Q85CG7
 ID Q65CG7 PRELIMINARY; PRT; 11 AA.
 AC Q65CG7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Transcriptional activator (Fragment).
 GN Name=AC2;
 OS Sinloa tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=71186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NI3.
 RA Rojas A., Kvarnheden A., Rodriguez D., Valkonen J.P.T.;
 RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in
 RT Nicaragua."
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ508781; CAD48523.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1356 MW; 861BC90602D379D5 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPFSLEWT 11
 Db 4 SPWVELFS 11

RESULT 12
 O46664
 ID O46664 PRELIMINARY; PRT; 12 AA.
 AC O46664;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glucose-6-phosphate dehydrogenase (Fragment).
 GN Name=G6PD;
 OS Macropus robustus robustus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OC NCBI_TaxID=35580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224585; PubMed=9060417;
 RA Loebel D.A., Johnston P.G.;
 RT "Analysis of the intron-exon structure of the G6PD gene of the
 RT wallaroo (Macropus robustus) by polymerase chain reaction."
 RL Mamm. Genome 8:146-147(1997).
 DR EMBL; U53774; AAC48789.1; --
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1430 MW; D42A9C84E3CB1AA9 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GSFFSE 8
 Db 2 GGYFDE 7

RESULT 13
 Q61331
 ID Q61331 PRELIMINARY; PRT; 12 AA.
 AC Q61331;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE N-acetylglucosamine beta-4 galactosyl transferase (EC 2.4.1.90)
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89033997; PubMed=3141392;
 RA Nakazawa K., Ando T., Kimura T., Narimatsu H.;
 RT "Cloning and sequencing of a full-length cDNA of mouse N-
 RT acetylglucosamine (beta 1-4)galactosyltransferase."
 RL J. Biochem. 104:165-168(1988).
 DR EMBL; D00315; BAA0217.1; --
 DR GO; GO:0003945; P:N-acetylglucosamine synthase activity; IEA.
 DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
 KW Glycosyltransferase; Transferase.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 WTS 12
 Db 1 WTS 3

RESULT 14
 FARP_MONEY
 ID FARP_MONEY STANDARD; PRT; 6 AA.
 AC P41966;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMPamide-like neuropeptide GNFRF-amide.
 OS Moniezia expansa (Sheep tapeworm).
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidae; Anoplocephalidae; Moniezia.
 OC NCBI_TaxID=28841;

```

RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRTamide: a novel FMRFamide-immunoreactive peptide isolated from
RL the sheep tapeworm, Moniezia expansa."; 1054-1060(1993).
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR: A43129; A43129.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 6 Phenylalanine amide.
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSFF 6
Db 1 GNFF 4

RESULT 15
Q99MNO
AC Q99MNO PRELIMINARY; PRT; 8 AA.
DT 01-JUN-2001 (TRENDELrel. 17, Created)
DT 01-JUN-2001 (TRENDELrel. 17, Last sequence update)
DE 01-DEC-2001 (TRENDELrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
GN Name=Adat1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=21231131; PubMed=11331948;
RA Maas S., Kim Y.G., Rich A.;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
RL tRNA synthetases.";
RL Mamm. Genome 12:387-393(2001).
DR EMBL: AF328904; AAK19310.1; -.
DR MGD; MGI:1353631; Adat1.
FT NON_TER 8
SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;

Query Match 28.4%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 LWTs 12
Db 1 MWTA 4

```

Search completed: April 27, 2005, 15:46:23
Job time : 176 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:39:49 ; Search time 167 Seconds
(without alignments)
27.791 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFFSELWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	82.1	12	AAB86005	AAB86005 DCM-assoc
2	34	50.7	6	AAB97294	Aab97294 Betal-adr
3	34	50.7	6	AAM47222	Aam47222 Dilated c
4	34	50.7	6	ADP49242	Adp49242 Disease-a
5	34	50.7	8	ABO9130	ABO9130 Hepatitis
6	31	46.3	10	ADK09671	Adk09671 Human pap
7	31	46.3	10	ADK09188	Adk09188 Human pap
8	30	44.8	6	ABR46515	ABr46515 Staphyloc
9	30	44.8	9	AAW72493	AAw72493 Dengue vi
10	30	44.8	10	AAW76040	AAw76040 LM609 gra
11	30	44.8	10	AAW37198	AAw37198 Human onc
12	30	44.8	10	ABE61398	ABe61398 Multiple
13	30	44.8	10	ABO19836	ABo19836 Enhanced
14	30	44.8	10	ADG71874	Adg71874 Enhanced
15	30	44.8	10	ADJ58055	Adj58055 Murine LM
16	29	43.3	7	AAV33139	AAv33139 Rabbit ca
17	29	43.3	10	AAU93215	AAu93215 Granulocy
18	29	43.3	11	ABJ37125	ABj37125 Rhodopsin
19	29	43.3	12	AAM00568	AAM00568 Human str
20	28	41.8	6	ABR46459	ABr46459 Staphyloc
21	28	41.8	7	ADr68302	ADr68302 Androgen
22	28	41.8	8	ADK09492	Adk09492 Human pap
23	28	41.8	9	AAV04678	AAv04678 Peptide #
24	28	41.8	9	ADK09532	Adk09532 Human pap
25	28	41.8	9	ADK09531	Adk09531 Human pap

26	28	41.8	9	8	ADK09533	Adk09533 Human pap
27	28	41.8	10	4	ABB55959	ABb55959 Vascular
28	28	41.8	10	8	ADK09606	Adk09606 Human pap
29	28	41.8	11	3	AAV93379	AAv93379 Binding m
30	28	41.8	11	7	ADP53467	ADp53467 MCPC 603
31	27.5	41.0	9	2	AAr58533	AAr58533 Light cha
32	27.5	41.0	9	2	AAr95306	AAr95306 Light cha
33	27	40.3	6	2	AAr89913	AAr89913 P53/MDM2
34	27	40.3	6	2	AAW13606	AAw13606 P53 prote
35	27	40.3	6	3	AAAB17074	AAa17074 Mdm/hdm a
36	27	40.3	6	5	ABB73169	ABb73169 Mdm/hdm a
37	27	40.3	6	6	ABR46627	ABr46627 Staphyloc
38	27	40.3	6	6	ABR46507	ABr46507 Staphyloc
39	27	40.3	6	6	ABG73432	ABg73432 Human p53
40	27	40.3	6	8	ADJ73323	ADj73323 Mdm/hdm a
41	27	40.3	6	8	ADJ52957	ADj52957 CH1 delet
42	27	40.3	6	8	ADJ51918	ADj51918 CH1 delet
43	27	40.3	7	2	AAr89921	AAr89921 Antibody
44	27	40.3	7	2	AAr89925	AAr89925 P53 bindi
45	27	40.3	7	3	AAy57789	AAy57789 TRAM-ince

ALIGNMENTS

RESULT 1
AAB86005
ID AAB86005 standard; peptide; 12 AA.
XX
AC AAB86005;
XX
DT 12-JUL-2001 (first entry)
XX
DE DCM-associated peptide #5.
XX
KW DCM; dilatative cardiomyopathy; autoantibody; cardiatic;
KW beta-1 adrenergic activated antibody; immunosuppressive.
XX
OS Synthetic.
XX
PN WO200121660-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-EP009241.
XX
PR 21-SEP-1999; 99EP-00118630.
PR 21-SEP-1999; 99EP-00118631.
XX
XX (APFI-) AFFINA IMMUNTECHNIK GMBH.
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX WPI; 2001-335469/35.
XX
XX New peptide useful for combating the autoantibodies that are responsible
XX for dilatative cardiomyopathy.
XX
XX Claim 3; Page 20; 29pp; German.
XX
XX This invention describes a novel peptide (P1) which can be used for (1)
XX isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
XX phase; and (2) a chromatographic apparatus with (P1) bound. The products
XX of the invention have cardiant and immunosuppressive activity. (P1) is
XX used to produce medicine to combat beta 1 adrenergic activated
XX autoantibodies having a causal pathological relationship with dilatative
XX cardiomyopathy. This sequence represents a specifically claimed peptide
XX used to illustrate the method of the invention
XX
XX Sequence 12 AA;

Query Match 92.1%; Score 55; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSFFSELWTS 12
 Db 2 GSFFSELWTS 11

RESULT 2
 AAB97294
 ID AAB97294 standard; peptide; 6 AA.

XX
 AC AAB97294;
 XX
 DT 13-AUG-2001 (first entry)
 XX

DE Betal-adrenoceptor secondary loop epitope peptide #3.

XX B cell; toxin; antigen specific; antibody mediated disease; virucide;
 KW immunosuppressive; antiinflammatory; antiallergic; antidiabetic;
 KW thyromimetic; antithyroid; vasotropic; cardiac; antitumor;
 KW neuroprotective; antirheumatic; antiarthritic; dermatological;
 KW ophthalmological; nephrotropic; allergy; autoimmune disorder;
 KW skin diseases; autoimmune endocrinopathy; vasculitic syndrome;
 KW cardiovascular disease; immunohaematologic disorder; neurologic disease;
 KW gastrointestinal disease; collagen vascular disease; renal diseases;
 KW pulmonary disease; infertility disorder; betal-adrenoceptor;
 KW dilated cardiomyopathy.

XX Unidentified.
 OS
 XX
 XX WO200132853-A1.
 PN
 XX
 XX 10-MAY-2001.
 PD
 XX
 XX 12-OCT-2000; 2000WO-US028157.
 PF
 XX
 XX 29-OCT-1999; 99US-0162464P.
 PR
 XX (BIOM-) INST APPLIED BIOMEDICINE.
 PA
 XX Chaplin JW;
 PI
 XX WPI; 2001-316435/33.
 DR
 XX

PT B cell clonal toxin useful for treating autoimmune disorders such as
 PT Grave's disease, myocardial infarction, Crohn's disease, multiple
 PT sclerosis, comprises a group that causes toxin to be internalized by B
 PT cell.

XX Disclosure; Page 26; 46pp; English.

CC This invention relates to a B cell clonal toxin. The toxin is made from
 CC two moieties, the first causes the toxin to be internalized by a B cell,
 CC and the second is a biologically acceptable toxin. The invention includes
 CC a method for inactivating/killing an antigen specific B cell. A target B
 CC cell is contacted with an effective amount of a B cell clonal toxin. The
 CC method is useful for selective immunosuppression in conditions
 CC characterised by the presence of an unwanted or deleterious immune
 CC response, e.g. in the treatment of antigen specific antibody mediated
 CC disease conditions. Use of the B cell clonal toxin can result in
 CC immunosuppressive; antiinflammatory; antiallergic; virucide; antidiabetic
 CC ; thyromimetic; antithyroid; vasotropic; cardiac; antitumor;
 CC neuroprotective; antirheumatic; antiarthritic; dermatological;
 CC ophthalmological; and nephrotropic activity. The toxin is particularly
 CC useful for treating a host suffering from an antigen specific antibody
 CC mediated disease condition, where the antigen specific antibody is
 CC produced by an antigen-reactive B cell population present in a host. The
 CC toxin is useful for treating allergies, viral disease conditions, and
 CC autoimmune disorders. Also treated are skin diseases; autoimmune
 CC autoimmunopathies; vasculitic syndromes; cardiovascular disease;
 CC immunohaematologic disorders; gastrointestinal diseases; neurologic
 CC diseases; collagen vascular diseases; renal diseases; pulmonary diseases;
 CC and infertility disorders. The present sequence represents a betal-

CC adrenoceptor epitope. An antibody response to this antigen is implicated
 CC in dilated cardiomyopathy, a disorder which may be treated using the
 CC toxin of the invention

XX
 SQ Sequence 6 AA;

Query Match 50.7%; Score 34; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFF 6
 Db 1 EYGSFF 6

RESULT 3
 AAM47222
 ID AAM47222 standard; peptide; 6 AA.

XX
 AC AAM47222;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Dilated cardiomyopathy adsorbents related peptide #2.
 XX
 KW Dilated cardiomyopathy; adsorbent; betal adrenoceptor;
 KW M2 muscarine receptor; antibody.
 XX
 OS Synthetic.
 XX
 XX WO200176662-A1.
 PN
 XX
 XX 18-OCT-2001.
 PD
 XX
 XX 09-APR-2001; 2001WO-JP003026.
 PF
 XX
 XX 07-APR-2000; 2000JP-00106915.
 PR
 XX (KANF) KANEKA CORP.
 PA
 XX Ogino E, Furuyoshi S, Hirai F, Nishimoto T;
 PI
 XX WPI; 2002-041274/05.
 DR
 XX Adsorbents for dilated cardiomyopathy, comprises an immobilized compound
 PT capable of selectively removing antibodies against approximately bi
 PT adrenoceptor and/or M2 muscarine receptors in body fluid without
 PT pretreatment.

XX Claim 3; Page 21; 37pp; Japanese.

CC The present invention relates to a method of immobilising an adsorbent
 CC with a compound capable of binding to an antibody against betal
 CC adrenoceptor and/or an antibody against M2 muscarine receptor on a
 CC water-insoluble support. The adsorbents, apparatus and method are useful
 CC for treating dilated cardiomyopathy by removing antibodies against betal
 CC adrenoceptor and/or M2 muscarine receptor. The present sequence is a
 CC peptide described in the exemplification of the invention

XX
 SQ Sequence 6 AA;

Query Match 50.7%; Score 34; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFF 6
 Db 1 EYGSFF 6

RESULT 4
 ADP49242
 ID ADP49242 standard; peptide; 6 AA.

```

XX AC ADP49242;
XX XX
XX DT 09-SEP-2004 (first entry)
XX XX
XX DE Disease-associated autoantibody detection method peptide #1.
XX XX
XX KW cardiant; gynaecological; immunosuppressive; hypotensive; antipsoriatic;
XX KW vasotropic; disease-associated autoantibody; antibody;
XX OS G protein-coupled receptor.
XX OS Unidentified.
XX XX
XX PN WO2004051280-A2.
XX XX
XX PD 17-JUN-2004.
XX XX
XX PF 28-NOV-2003; 2003WO-DE003988.
XX XX
XX PR 29-NOV-2002; 2002DE-01056897.
XX PR 27-JAN-2003; 2003DE-01003120.
XX PR 13-JUN-2003; 2003DE-01027066.
XX XX
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX XX
XX PI Wallukat G;
XX XX
XX DR WPI; 2004-450802/42.
XX XX
XX PT Detecting disease-associated autoantibodies against G protein-coupled
XX PT receptors, useful for diagnosing e.g. cardiomyopathy, comprises an
XX PT enzymatic or color reaction.
XX PS Claim 12; Page 49; 57pp; German.
XX XX
XX CC The present invention relates to a method for detecting disease-
XX CC associated autoantibodies (AAb) directed against G protein-coupled
XX CC receptors. This comprises treating a body fluid with a denaturing agent,
XX CC treating the precipitate formed with a biotin-containing peptide having
XX CC the (partial) sequence of a first and/or second loop of a G protein-
XX CC coupled receptor, incubating the mixture with a carrier coated by
XX CC (strept)avidin, washing the carrier and incubating it with labeled anti-
XX CC immunoglobulin G (IgG) antibody subclasses, and performing an enzymatic
XX CC or colour reaction. The method is used to detect AAb associated with
XX CC dilatative or Chagas cardiomyopathy, myocarditis, pre-eclampsia, humoral
XX CC kidney rejection, malignant, essential, refractory or pulmonary
XX CC hypertension, psoriasis and Reynaud's syndrome. The present invention is
XX CC a peptide which can be used in the method of the invention.
XX SQ
XX Query Match 50.7%; Score 34; DB 8; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFF 6
Db 1 EYGSFF 6

RESULT 5
AAB09130
ID AAB09130 standard; protein; 8 AA.
XX AC
XX AC AAB09130;
XX XX
XX DT 06-AUG-2003 (revised)
XX DT 30-AUG-2000 (first entry)
XX XX
XX DE Hepatitis GB virus protein sequence SEQ ID NO:252.
XX XX
XX KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
XX KW detection; characterisation; hepatitis.

XX OS Hepatitis GB virus.
XX OS US6051374-A.
XX PN 18-APR-2000.
XX PD
XX PF 07-JUN-1995; 95US-00488445.
XX PR 14-FEB-1994; 94US-00196030.
XX PR 13-MAY-1994; 94US-00242654.
XX PR 29-JUL-1994; 94US-00283314.
XX PR 23-NOV-1994; 94US-00344185.
XX PR 23-NOV-1994; 94US-00344190.
XX PR 30-JAN-1995; 95US-00377557.
XX XX
XX PA (ABBO ) ABBOTT LAB.
XX XX
XX PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
XX PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX XX
XX DR WPI; 2000-338307/29.
XX XX
XX PT Detecting target hepatitis GB virus nucleic acid in a test sample
XX PT suspected of containing HGBV comprises reacting the test sample the HGBV
XX PT polynucleotide probe and detecting the complex that contains target HGBV.
XX XX
XX PS Example 9; Col 331-332; 369pp; English.
XX XX
XX CC The present invention describe a method for detecting target hepatitis GB
XX CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
XX CC containing HGBV. The method involves reacting (T) with a HGBV
XX CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
XX CC selectively hybridises to the HGBV genome or its full complement, and
XX CC detecting the complex that contains THN, indicating the presence of
XX CC target HGBV. The method is used for detecting target HGBV nucleic acid in
XX CC the test sample suspected of containing HGBV and for characterisation of
XX CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
XX CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
XX CC AAM55270 to AAM55489 and AAB08985 to AAB09480 represent nucleotide and
XX CC protein sequences used in the exemplification of the present invention.
XX CC (Updated on 06-AUG-2003 to correct OS field.)
XX SQ
XX Query Match 50.7%; Score 34; DB 3; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FSELWTS 12
Db 1 FSHLWTS 7

RESULT 6
ADK09671
ID ADK09671 standard; peptide; 10 AA.
XX AC
XX AC ADK09671;
XX XX
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #1726.
XX XX
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX PN WO2004011650-A2.
XX XX
XX PD 05-FEB-2004.
XX XX

```

PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 FR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX WPI; 2004-169243/16.
 XX
 DR New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 18; Page 192; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX
 SQ Sequence 10 AA;
 Query Match 46.3%; Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 SPFSSELTWT 11
 Db ||||| :
 1 SPFSRTWS 8
 RESULT 7
 ADK09188
 ID ADK09188 standard; peptide; 10 AA.
 XX
 AC ADK09188;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human papillomavirus peptide #1243.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 XX
 OS Human papillomavirus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX WPI; 2004-169243/16.
 XX
 DR New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 18; Page 187; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX
 SQ Sequence 10 AA;
 Query Match 46.3%; Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 SPFSSELTWT 11
 Db ||||| :
 1 SPFSRTWS 8
 RESULT 8
 ABR46515
 ID ABR46515 standard; peptide; 6 AA.
 XX
 AC ABR46515;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #1705.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 17; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;

Query Match 44.8%; Score 30; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 FFESEW 10
 DB 1 FFESEW 6

RESULT 9

AAW72493
 ID AAW72493 standard; peptide; 9 AA.

XX
 AC AAW72493;

DT 23-DEC-1998 (first entry)

DE Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #39.

XX Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;
 KW dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;
 KW immunisation; immunoreactive; infection.

XX Dengue virus.

OS US5824506-A.

XX 20-OCT-1998.

XX 15-AUG-1994; 94US-00290268.

XX 15-AUG-1994; 94US-00290268.

XX (GENE-) GENELABS DIAGNOSTICS PTE LTD.

XX Chan L, Guan M;

XX WPI; 1998-582552/49.

XX Dengue virus peptide antigens - especially for diagnosis of dengue virus
 PT infection.

XX Example 1; Col 17; 21pp; English.

XX AAW72456 to AAW72570 represent peptide fragments from the dengue virus
 CC type-2 glycoprotein NS1, which was used in an example from the present
 CC invention for an epitope mapping assay. The invention has developed
 CC peptide antigens consisting of fragments of the dengue virus NS1 protein.
 CC The peptide antigens can be used for the diagnosis of dengue virus
 CC infection by detection of antibodies to the virus, especially in an assay
 CC comprising attaching the antigen to a solid support, contacting a serum
 CC sample with the support, and detecting bound antibodies with a labelled
 CC anti-human antibody or used for preparing vaccines against dengue virus
 CC infection

XX Sequence 9 AA;

Query Match 44.8%; Score 30; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GSFFSELW 10

DB 1 GVFFFTNIW 8

RESULT 10

AAW76040

ID AAW76040 standard; protein; 10 AA.

XX
 AC AAW76040;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #16.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US001826.

XX 30-JAN-1997; 97US-00791391.

XX (IXSY-) IXSYS INC.

XX Huse WD, Glaser SM;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49877.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis.

XX Claim 62; Page 43; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block integrin-
 CC mediated signal transduction. This is useful in the treatment, prevention
 CC and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis
 CC and restenosis (but also e.g. (non-)immune inflammation, diabetic
 CC retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody

XX Sequence 10 AA;

Query Match 44.8%; Score 30; DB 2; Length 10;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFSPS 7

DB 5 YGSFYS 10

RESULT 11

AAW37198

ID AAW37198 standard; peptide; 10 AA.

XX
 AC AAW37198;

XX 20-JUL-1998 (first entry)

XX

DE Human oncogenic protein MDM2 binding Cys (Acrlid) peptide derivative 2.
 XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumour; diagnosis; binding; viral infection.
 XX Synthetic.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; Sulphydryl side-chain linked
 FT to 6-acryloyl-2-(dimethylamino) naphthalene"
 FT Modified-site 10
 FT /note= "C-terminal amide"
 FT
 XX WO9801467-A2.
 PN
 XX 15-JAN-1998.
 PD
 XX
 XX 04-JUL-1997; 97WO-EP003549.
 PF
 XX
 XX 05-JUL-1996; 96GB-00014197.
 PR
 XX 07-APR-1997; 97GB-00007041.
 PR
 XX (NOVS) NOVARTIS AG.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA
 XX Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 PI WPI; 1998-100996/09.
 DR
 XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 PT
 XX Example 2; Page 20; 45pp; English.
 PS
 XX This is a Cys (Acrlid) peptide derivative capable of binding to a human
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC molecules that bind to MDM2 and to identify and design inhibitors of
 CC MDM2/p53 binding. They may also be used to purify binding partners
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC cancer and leukaemia patients and for treatment or prevention of disease
 CC involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 CC injection. By interfering with MDM2/p53 interaction, the peptides can
 CC activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53
 XX
 SQ Sequence 10 AA;
 Query Match 44.8%; Score 30; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GSFFSELW 10
 | | | | |
 Db 2 GPTFSDLW 9
 RESULT 12
 AAB61398
 ID AAB61398 standard; peptide; 10 AA.
 XX
 AC AAB61398;
 XX
 DT 03-APR-2001 (first entry)

DE Human oncogenic protein MDM2 binding Cys (Acrlid) peptide derivative 2.
 XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumour; diagnosis; binding; viral infection.
 XX Synthetic.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; Sulphydryl side-chain linked
 FT to 6-acryloyl-2-(dimethylamino) naphthalene"
 FT Modified-site 10
 FT /note= "C-terminal amide"
 FT
 XX WO9801467-A2.
 PN
 XX 15-JAN-1998.
 PD
 XX
 XX 04-JUL-1997; 97WO-EP003549.
 PF
 XX
 XX 05-JUL-1996; 96GB-00014197.
 PR
 XX 07-APR-1997; 97GB-00007041.
 PR
 XX (NOVS) NOVARTIS AG.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA
 XX Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 PI WPI; 1998-100996/09.
 DR
 XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 PT
 XX Example 2; Page 20; 45pp; English.
 PS
 XX This is a Cys (Acrlid) peptide derivative capable of binding to a human
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC molecules that bind to MDM2 and to identify and design inhibitors of
 CC MDM2/p53 binding. They may also be used to purify binding partners
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC cancer and leukaemia patients and for treatment or prevention of disease
 CC involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 CC injection. By interfering with MDM2/p53 interaction, the peptides can
 CC activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53
 XX
 SQ Sequence 10 AA;
 Query Match 44.8%; Score 30; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GSFFSELW 10
 | | | | |
 Db 2 GPTFSDLW 9
 RESULT 12
 AAB61398
 ID AAB61398 standard; peptide; 10 AA.
 XX
 AC AAB61398;
 XX
 DT 03-APR-2001 (first entry)

DE Multiple mutant VH CDR3 #4.
 XX
 XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 XX Unidentified.
 OS
 XX WO200078815-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US017454.
 PF
 XX 24-JUN-1999; 99US-00339922.
 PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Huse WD, Wu H;
 PI
 XX WPI; 2001-050110/06.
 DR
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.
 PT
 XX Disclosure; Page 43; 132pp; English.
 PS
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or their
 CC functional fragments. The antibodies or their functional fragments can be
 CC used in the diagnosis and treatment of alphaVbeta3-mediated diseases
 CC such as angiogenesis, inflammatory diseases (such as psoriasis and
 CC chronic articular rheumatism), disorders associated with inappropriate or
 CC inopportune invasion of vessels (such as diabetic retinopathy,
 CC neovascular glaucoma and cancer disorders such as tumours and Kaposi's
 CC sarcoma), retinal diseases (such as macular degeneration), restenosis and
 CC osteoporosis
 XX
 SQ Sequence 10 AA;
 Query Match 44.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YGSFVS 7
 | | | | |
 Db 5 YGSFVS 10
 RESULT 13
 ABO19836
 ID ABO19836 standard; peptide; 10 AA.
 XX
 AC ABO19836;
 XX
 XX 28-AUG-2003 (first entry)
 DT
 XX Enhanced LM609 heavy chain variable region CDR3 #15.
 DE
 XX LM609; antibody; grafted antibody; alpha vbeta3; angiogenesis; CDR;
 KW alpha.vbeta_3-mediated disease; complementarity determining region;
 KW restenosis.
 XX
 XX Unidentified.
 OS
 XX US2003028009-A1.
 PN
 XX 06-FEB-2003.
 PD
 XX 06-JUL-2001; 2001US-00900590.
 PF
 XX

PR 30-JAN-1998; 98US-00016061.
 XX (IXSY-) IXSYS INC.
 PA Huse WD;
 XX WPI; 2003-492042/46.
 DR N-PSDB; ACD30195.
 XX New Vitaxin or LM609 grafted antibody exhibiting selective binding
 PT affinity to alphavbeta3, useful for treating an alphavbeta3-mediated
 PT disease e.g., angiogenesis or restenosis.
 XX Claim 62; Page 13; 71pp; English.
 PS The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting
 CC selective binding affinity to alpha.vbeta.3. The Vitaxin or LM609 grafted
 CC antibody is useful for treating an alpha.vbeta.3-mediated disease e.g.
 CC angiogenesis or restenosis. The present sequence represents the amino
 CC acid sequence of a LM609 complementarity determining region
 XX Sequence 10 AA;
 SQ

Query Match 44.8%; Score 30; DB 6; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YGSFYS 7
 DB ||||:|
 5 YGSFYS 10

RESULT 14
 ADG71874
 ID ADG71874 standard; protein; 10 AA.
 AC ADG71874;
 XX 11-MAR-2004 (first entry)
 DT Enhanced LM609 grafted antibody VH region CDR3 #15.
 DE LM609 grafted antibody; high affinity; alphavbeta3;
 XX complementarity determining region; CDR; inflammatory disorder;
 KW immune inflammation; non-immune inflammation;
 KW chronic articular rheumatism; psoriasis; vessel disorder;
 KW diabetic retinopathy; neovascular glaucoma; capillary proliferation;
 KW atherosclerotic plaque; cancer disorder; antiinflammatory; antirheumatic;
 KW dermatological; immunosuppressive; ophthalmological; humanised.
 XX Synthetic.
 OS Homo.sapiens.
 OS US6596850-B1.
 PN 22-JUL-2003.
 XX 30-JAN-1998; 98US-00016061.
 XX 30-JAN-1998; 98US-00016061.
 XX (IXSY-) IXSYS INC.
 PA Huse WD;
 XX WPI; 2003-842325/78.
 DR N-PSDB; ADG71873.
 XX New high affinity LM609 grafted antibody exhibiting selective binding to
 PT alphav-beta3, useful for treating inflammatory disorders such as immune
 PT and non-immune inflammation, chronic articular rheumatism, psoriasis.
 XX Claim 6; SEQ ID NO 100; 66pp; English.

XX The present invention relates to a high affinity LM609 grafted antibody
 CC exhibiting selective binding to alphavbeta3, or its functional fragment
 CC comprising one or more complementarity determining regions (CDRs) having
 CC at least one amino acid substitution in one or more CDRs of the LM609
 CC grafted heavy chain variable region of a polypeptide having 117 amino
 CC acids or a grafted light chain variable region polypeptide having 107
 CC amino acids. Also disclosed are polynucleotide sequences encoding the
 CC novel antibody or its functional fragment, and a composition comprising
 CC the novel antibody or its functional fragment. The antibodies and their
 CC fragments are useful for treating alphavbeta3-mediated diseases, e.g.
 CC inflammatory disorders such as immune and non-immune inflammation,
 CC chronic articular rheumatism, psoriasis, disorders associated with
 CC inappropriate or inopportune invasion of vessels such as diabetic
 CC retinopathy, neovascular glaucoma, and capillary proliferation in
 CC atherosclerotic plaques as well as cancer disorders. The present sequence
 CC represents an antibody region.
 XX Sequence 10 AA;
 SQ

Query Match 44.8%; Score 30; DB 7; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YGSFYS 7
 DB ||||:|
 5 YGSFYS 10

RESULT 15
 ADJ58055
 ID ADJ58055 standard; peptide; 10 AA.
 XX AC ADJ58055;
 XX 06-MAY-2004 (first entry)
 DT Murine LM609 heavy chain variable region (VH) CDR3 mutant peptide #15.
 DE Vitaxin; antibody; LM609; angiogenesis; restenosis; therapy;
 KW variable region; mouse; mutant; mutein.
 XX Mus sp.
 OS Synthetic.
 OS US2004006213-A1.
 PN 08-JAN-2004.
 XX 16-JUN-2003; 2003US-00463847.
 XX 30-JAN-1997; 97US-00791391.
 PR 30-JAN-1998; 98US-00016061.
 XX (IXSY-) IXSYS INC.
 PA Huse WD, Glaser SM;
 XX WPI; 2004-081749/08.
 DR New Vitaxin antibody and a LM609 grafted antibody exhibiting selective
 PT binding affinity to alphavbeta3, useful for treating alphavbeta3-mediated
 PT diseases, e.g. angiogenesis or restenosis.
 XX Claim 62; SEQ ID NO 100; 69pp; English.
 PS The present invention provides a Vitaxin antibody and a LM609 grafted
 CC antibody exhibiting selective binding affinity to alpha-v-beta-3. The
 CC invention is useful for treating alpha-v-beta-3-mediated diseases such as
 CC angiogenesis and restenosis. The present sequence is murine LM609
 CC antibody variable region CDR mutant peptide.
 XX Sequence 10 AA;
 SQ

Query Match 44.8%; Score 30; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFFS 7
| | | | |
Db 5 YGSFYS 10

Search completed: April 27, 2005, 15:49:16
Job time : 169 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:40:23 ; Search time 41 Seconds
(without alignments)
21.849 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFFSELWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:**
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:**
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:**
- 5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	50.7	8	4	US-08-469-260A-252
2	34	50.7	8	4	US-08-469-260A-252
3	34	50.7	8	4	US-08-469-260A-252
4	34	50.7	8	4	US-08-469-260A-252
5	30	44.8	6	1	US-08-424-957-6
6	30	44.8	6	3	US-09-035-686-6
7	30	44.8	10	4	US-09-339-922A-100
8	30	44.8	10	4	US-09-016-061-100
9	30	44.8	11	1	US-08-424-957-42
10	30	44.8	11	3	US-09-035-686-42
11	29	43.3	7	4	US-09-595-682B-10
12	29	43.3	10	4	US-09-620-091-28
13	28	41.8	11	3	US-09-186-958-6
14	28	41.8	11	3	US-09-669-271A-6
15	28	41.8	11	4	US-09-881-276-6
16	27.5	41.0	9	1	US-08-931-645-50
17	27.5	41.0	9	3	US-08-300-386A-50
18	27.5	41.0	9	5	PCT-US94-01258-50
19	27.5	41.0	9	5	PCT-US95-11235-50
20	27	40.3	6	1	US-08-277-660A-2
21	27	40.3	6	1	US-08-424-957-2
22	27	40.3	6	3	US-09-035-686-2
23	27	40.3	6	4	US-09-081-975-1
24	27	40.3	6	4	US-09-428-082B-130
25	27	40.3	6	4	US-09-732-384-4
26	27	40.3	7	1	US-08-277-660A-27
27	27	40.3	7	1	US-08-424-957-15

28	27	40.3	7	1	US-08-424-957-19	Sequence 19, Appl
29	27	40.3	7	3	US-09-035-686-15	Sequence 15, Appl
30	27	40.3	7	3	US-09-035-686-19	Sequence 19, Appl
31	27	40.3	10	1	US-08-277-660A-7	Sequence 7, Appl
32	27	40.3	10	1	US-08-424-957-11	Sequence 11, Appl
33	27	40.3	10	1	US-08-424-957-18	Sequence 18, Appl
34	27	40.3	10	3	US-09-035-686-11	Sequence 11, Appl
35	27	40.3	10	3	US-09-035-686-18	Sequence 18, Appl
36	27	40.3	11	1	US-08-277-660A-9	Sequence 9, Appl
37	27	40.3	11	1	US-08-277-660A-10	Sequence 10, Appl
38	27	40.3	11	1	US-08-277-660A-11	Sequence 11, Appl
39	27	40.3	11	1	US-08-277-660A-12	Sequence 12, Appl
40	27	40.3	11	1	US-08-277-660A-13	Sequence 13, Appl
41	27	40.3	11	1	US-08-277-660A-19	Sequence 19, Appl
42	27	40.3	11	1	US-08-277-660A-20	Sequence 20, Appl
43	27	40.3	11	1	US-08-424-957-17	Sequence 17, Appl
44	27	40.3	11	1	US-08-424-957-23	Sequence 23, Appl
45	27	40.3	11	1	US-08-424-957-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAM J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROPP
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-469-260A-252

Query Match 50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
|||
Db 1 FSHLWTS 7

RESULT 2

US-08-488-446-252
; Sequence 252, Application US/08488446
; Patent No. 6558898

GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: JAMES C. ERKER

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,446

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: FOREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-446-252

Query Match 50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
|||
Db 1 FSHLWTS 7

RESULT 3

US-08-467-344A-252

; Sequence 252, Application US/08467344A
; Patent No. 6586568

GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: JAMES C. ERKER

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,344A

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/424,550

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: FOREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 252:

US-08-467-344A-252

Query Match 50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
|||
Db 1 FSHLWTS 7

RESULT 4

US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Patent No. 6720166

GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELTWS 12
Db 1 FSHLWTS 7

RESULT 5
US-08-424-957-6
Sequence 6, Application US/08424957
Patent No. 5770377
GENERAL INFORMATION:
APPLICANT: Pickseley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WH/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-6

Query Match 44.8%; Score 30; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELTW 10
Db 2 FSELTW 6

RESULT 6
US-09-035-686-6
Sequence 6, Application US/09035686
Patent No. 6153391
GENERAL INFORMATION:
APPLICANT: Pickseley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,686
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WH/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-035-686-6

Query Match 44.8%; Score 30; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 6 FSELM 10
Db 2 FSELM 6

RESULT 7
US-09-339-922A-100
; Sequence 100, Application US/09339922A
; Patent No. 6531580
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-100

Query Match 44.8%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFYS 7
Db 5 YGSFYS 10

RESULT 8
US-09-016-061-100
; Sequence 100, Application US/09016061
; Patent No. 6596850
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-100

Query Match 44.8%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFYS 7
Db 5 YGSFYS 10

RESULT 9
US-08-424-957-42
; Sequence 42, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-42

Query Match 44.8%; Score 30; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELM 10
Db 5 YGSFYS 10

Db 5 FSELW 9

RESULT 10
US-09-035-686-42
; Sequence 42, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickstley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hombach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-42

Query Match 44.8%; Score 30; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELW 10
Db 5 FSELW 9

RESULT 11
US-09-595-682B-10
; Sequence 10, Application US/09595682B
; Patent No. 6800483
; GENERAL INFORMATION:
; APPLICANT: Danks, Mary K.
; APPLICANT: Potter, Philip M.
; APPLICANT: Houghton, Peter J.
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
; TITLE OF INVENTION: Tumor Cells
; FILE REFERENCE: SJ-0005
; CURRENT APPLICATION NUMBER: US/09/595,682B
; CURRENT FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: 60/075,258

Query Match 43.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFFSELW 10
Db 1 AFWIELW 7

RESULT 12
US-09-620-091-28
; Sequence 28, Application US/09620091
; Patent No. 6716811
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DURFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/09/620,091
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-620-091-28

Query Match 43.3%; Score 29; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SFFSELW 10
Db 3 SFWVELW 9

RESULT 13
US-09-186-958-6
; Sequence 6, Application US/09186958B
; Patent No. 6238860
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayette
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/186,958B
; CURRENT FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; OTHER INFORMATION: binding polypeptide
US-09-186-958-6

Query Match 41.8%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFESEWTS 12
|||
Db 1 FFCALWPS 8

RESULT 14

US-09-669-271A-6
; Sequence 6, Application US/09669271A
; Patent No. 6291197
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Faville
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/669,271A
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; OTHER INFORMATION: binding polypeptide
US-09-669-271A-6

Query Match 41.8%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFESEWTS 12
|||
Db 1 FFCALWPS 8

RESULT 15

US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. 6479641
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Faville
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polype
US-09-881-276-6

Query Match 41.8%; Score 28; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFESEWTS 12
|||
Db 1 FFCALWPS 8

Search completed: April 27, 2005, 15:50:02
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:46:39 ; Search time 138 Seconds
(without alignments)
28.938 Million cell updates/sec

Title: US-10-088-681-2
Perfect score: 67
Sequence: 1 EYGSFPELWTS 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 211037

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	50.7	6	16	US-10-221-042-2
2	34	50.7	8	8	US-08-424-550B-252
3	30	44.8	10	9	US-09-214-371-35
4	30	44.8	10	9	US-09-214-371-36
5	30	44.8	10	10	US-09-900-590-100
6	30	44.8	10	14	US-10-305-231-100
7	30	44.8	10	15	US-10-463-847-100
8	29	43.3	10	17	US-10-659-207-28
9	28	41.8	9	9	US-09-486-734A-35
10	28	41.8	11	9	US-09-881-276-6
11	28	41.8	11	15	US-10-417-895A-56
12	27	40.3	6	9	US-09-214-371-83
13	27	40.3	6	9	US-09-732-384-4

14	27	40.3	6	13	US-10-155-059-1	Sequence 1, Appli
15	27	40.3	6	15	US-10-609-217-130	Sequence 130, App
16	27	40.3	6	15	US-10-632-388-130	Sequence 130, App
17	27	40.3	6	15	US-10-651-723-130	Sequence 130, App
18	27	40.3	6	15	US-10-645-761-130	Sequence 130, App
19	27	40.3	6	15	US-10-686-696-130	Sequence 130, App
20	27	40.3	6	15	US-10-653-048-130	Sequence 130, App
21	27	40.3	8	16	US-10-340-179-2	Sequence 2, Appli
22	27	40.3	8	16	US-10-340-179-3	Sequence 3, Appli
23	27	40.3	9	9	US-09-214-371-37	Sequence 37, Appli
24	27	40.3	9	9	US-09-214-371-38	Sequence 38, Appli
25	27	40.3	9	16	US-10-340-179-1	Sequence 1, Appli
26	27	40.3	10	17	US-10-726-332-107	Sequence 107, App
27	27	40.3	11	10	US-09-840-085-31	Sequence 31, Appl
28	27	40.3	12	9	US-09-214-371-17	Sequence 17, Appl
29	27	40.3	12	9	US-09-214-371-24	Sequence 24, Appl
30	27	40.3	12	9	US-09-214-371-25	Sequence 25, Appl
31	27	40.3	12	15	US-10-609-217-131	Sequence 131, App
32	27	40.3	12	15	US-10-609-217-132	Sequence 132, App
33	27	40.3	12	15	US-10-609-217-143	Sequence 143, App
34	27	40.3	12	15	US-10-609-217-144	Sequence 144, App
35	27	40.3	12	15	US-10-632-388-131	Sequence 131, App
36	27	40.3	12	15	US-10-632-388-132	Sequence 132, App
37	27	40.3	12	15	US-10-632-388-143	Sequence 143, App
38	27	40.3	12	15	US-10-632-388-144	Sequence 144, App
39	27	40.3	12	15	US-10-651-723-131	Sequence 131, App
40	27	40.3	12	15	US-10-651-723-132	Sequence 132, App
41	27	40.3	12	15	US-10-651-723-143	Sequence 143, App
42	27	40.3	12	15	US-10-651-723-144	Sequence 144, App
43	27	40.3	12	15	US-10-645-761-131	Sequence 131, App
44	27	40.3	12	15	US-10-645-761-132	Sequence 132, App
45	27	40.3	12	15	US-10-645-761-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-10-221-042-2
; Sequence 2, Application US/10221042
; Publication No. US20040120946A1
; GENERAL INFORMATION:
; APPLICANT: KANEKA CORPORATION
; TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY
; FILE REFERENCE: 12218/5
; CURRENT APPLICATION NUMBER: US/10/221,042
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: PCT/JF01/03026
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: JP 2000-106915
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Peptide having a binding affinity for an antibody against
; OTHER INFORMATION: beta1-adrenoceptor and/or an antibody against M2 muscarinic recep
; OTHER INFORMATION: tor
US-10-221-042-2

Query Match 50.7%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYGSFP 6

Db 1 EYGSFP 6

RESULT 2
US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MURHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 50.7%; Score 34; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSESLWTS 12
Db 1 FSHLWTS 7

RESULT 3
US-09-214-371-35
; Sequence 35, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: x = Pro-NH2
US-09-214-371-35

Query Match 44.8%; Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFFSELM 10
Db 2 GPTFSDLW 9

RESULT 4
US-09-214-371-36
; Sequence 36, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: x = Ac-Cys
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: x = Pro-NH2
US-09-214-371-36

Query Match 44.8%; Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFFSELM 10
Db 2 GPTFSDLW 9

```

RESULT 5
US-09-900-590-100
; Sequence 100, Application US/09900590
; Publication No. US20030028009A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/900,590
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/016,061
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-900-590-100

Query Match 44.8%; Score 30; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
DB 5 YGSFYS 10

RESULT 6
US-10-305-231-100
; Sequence 100, Application US/10305231
; Publication No. US20030166872A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/10/305,231
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/09/339,922
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100

```

```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-10-305-231-100

Query Match 44.8%; Score 30; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
DB 5 YGSFYS 10

RESULT 7
US-10-463-847-100
; Sequence 100, Application US/10463847
; Publication No. US20040006213A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,847
; FILING DATE: 16-Jun-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-463-847-100

Query Match 44.8%; Score 30; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
DB 5 YGSFYS 10

```

RESULT 8

US-10-659-207-28
; Sequence 28, Application US/10659207
; Publication No. US20050037959A1
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/659,207
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-659-207-28

Query Match 43.3%; Score 29; DB 17; Length 10;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPFSELM 10
||: |||
Db 3 SPFWELW 9

RESULT 9

US-09-486-734A-35
; Sequence 35, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Ezlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; TITLE OF INVENTION: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 33339/196048
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HsdS subunit
US-09-486-734A-35

Query Match 41.8%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GSFFSEL 9
||: |||
Db 2 GSFFKQL 8

RESULT 10

US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. US20020031761A1
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Favelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polype
US-09-881-276-6

Query Match 41.8%; Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PFSELWTS 12
||: |||
Db 1 PFCALWPS 8

RESULT 11

US-10-417-895A-56
; Sequence 56, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Capuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-56

Query Match 41.8%; Score 28; DB 15; Length 11;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 SFFSELWTS 12
||: |||
Db 1 SYYSSSWSS 9

RESULT 12

```
US-09-214-371-83
; Sequence 83, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Ficksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
; OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83

Query Match 40.3%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELW 10
DB 2 FSDLW 6

RESULT 13
US-09-732-384-4
; Sequence 4, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jijie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-4

Query Match 40.3%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELW 10
DB 2 FSDLW 6

RESULT 14
US-10-155-059-1
; Sequence 1, Application US/10155059
; Publication No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERE TO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-155-059-1

Query Match 40.3%; Score 27; DB 13; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELW 10
DB 2 FSDLW 6

RESULT 15
US-10-609-217-130
; Sequence 130, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
```

Thu Apr 28 07:26:25 2005

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; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-130

Query Match      40.3%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 FSELW 10
      |||
Db      2 PSDLW 6

Search completed: April 27, 2005, 16:01:24
Job time : 139 secs
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